

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2000, 12:32:43 ; Search time 1178.81 Seconds
(without alignments)
6086.469 Million cell updates/sec

Title: US-09-142-471-1
Perfect score: 1627
Sequence: 1 gtcacgcagtgagtgtag.....gtacatgggcaccgtgac 1627

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues

Total number of hits satisfying chosen parameters: 10495684

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
30: gb_est11:*
31: gb_est12:*
32: gb_est13:*
33: gb_est14:*
34: gb_est15:*
35: gb_est16:*
36: gb_est17:*
37: gb_est18:*
38: gb_est19:*
39: gb_est20:*
40: gb_est21:*
41: gb_est22:*
42: gb_est23:*
43: gb_est24:*

44: gb_est25:*
45: gb_est26:*
46: gb_est27:*
47: gb_est28:*
48: gb_est29:*
49: gb_est30:*
50: gb_est31:*
51: gb_est32:*
52: em_est20:*
53: em_est21:*
54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*
59: gb_est33:*
60: gb_est34:*
61: gb_est35:*
62: gb_est36:*
63: gb_est37:*
64: gb_est38:*
65: em_est27:*
66: em_est28:*
67: em_est29:*
68: em_est30:*
69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_est45:*
80: gb_est46:*
81: gb_est47:*
82: em_est35:*
83: em_est36:*
84: em_est37:*
85: gb_est48:*
86: gb_est49:*
87: gb_est50:*
88: gb_est51:*
89: gb_est52:*
90: gb_est53:*
91: gb_est54:*
92: gb_est55:*
93: gb_gss1:*
94: gb_gss2:*
95: gb_gss3:*
96: gb_gss4:*
97: em_gss1:*
98: em_gss2:*
99: em_gss3:*
100: em_gss4:*
101: gb_gss5:*
102: gb_gss6:*
103: gb_gss7:*
104: gb_gss8:*
105: gb_gss9:*
106: em_gss5:*
107: em_gss6:*
108: em_gss7:*
109: em_gss8:*
110: em_gss9:*
111: em_gss10:*
112: em_gss11:*
113: gb_gss10:*
114: gb_gss11:*
115: em_gss12:*
116: gb_gss12:*

117: gb_gss13:*
118: gb_gss14:*
119: gb_gss15:*
120: gb_gss16:*
121: gb_gss17:*
122: gb_gss18:*
123: gb_gss19:*
124: em_gss13:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1		380	23.4	517	79	AW630744	W31016 hb87a03.y
2		372.2	22.9	595	91	W31016	W31016 zb85e08.r1
3		364	22.4	481	43	AI751501	AI751501 cn10c12.y
C 4		297.4	18.3	771	43	AI735329	AI735329 at09c06.x
C 5		286.4	17.6	731	35	AI085963	AI085963 o286h01.x
C 6		281	17.3	725	44	AI824041	AI824041 w129h07.x
C 7		248.6	15.3	287	89	T29234	T29234 EST73852 Hu
C 8		240.2	14.8	655	40	AI472218	AI472218 t186e02.x
C 9		216.4	13.3	280	25	AA381568	AA381568 EST94686
10		210	12.9	618	91	W51812	W51812 zc48h04.r1
11		186	11.4	311	25	AA381892	AA381892 EST95205
12		172.4	10.6	316	25	AA380919	AA380919 EST93950
C 13		169.2	10.4	594	38	AI343270	AI343270 tb94c07.x
C 14		148.2	9.1	311	79	AW630409	AW630409 hb76g07.y
15		139	8.5	628	47	AI982185	AI982185 pat.pk007
16		128	7.9	170	25	AA362308	AA362308 EST71834
C 17		125.6	7.7	463	43	AI751500	AI751500 cn10c12.x
C 18		106.2	6.5	525	33	AA947476	AA947476 ok20h06.s
19		95.6	5.9	498	28	AA553279	AA553279 vk82h10.s
C 20		91.2	5.6	562	30	AA721478	AA721478 n274g01.s
C 21		81	5.0	636	69	AW214008	AW214008 uo46e09.x
C 22		79.2	4.9	657	121	B87803	B87803 RPCI11-30H2
C 23		77	4.7	601	73	AW519504	AW519504 up33e08.y
C 24		76.6	4.7	416	94	AQ135450	AQ135450 HS_3053.A
25		74	4.5	196	25	AA381453	AA381453 EST94531
26		70.2	4.3	617	79	AW637075	AW637075 b154a09.w
C 27		65.8	4.0	923	35	AI095255	AI095255 oy18h07.s
C 28		58.4	3.6	925	122	CNS0091P	AL053013 Drosophil
C 29		53.2	3.3	473	35	AI074123	AI074123 o254c06.x
C 30		53	3.3	441	73	AW503691	AW503691 UI-HF-BNO
31		52.6	3.2	925	122	CNS0091P	AL053013 Drosophil
32		51.2	3.1	385	72	AW437358	AW437358 78370 MAR
C 33		51.2	3.1	464	69	AW243012	AW243012 xn28c05.x
C 34		50.2	3.1	839	122	CNS004NB	AL054280 Drosophil
C 35		49	3.0	645	122	CNS01213	AL101589 Drosophil
C 36		47.6	2.9	932	122	CNS0072Q	AL066742 Drosophil
37		47.2	2.9	935	122	CNS006KK	AL066051 Drosophil
38		47	2.9	1101	123	CNS017SY	AL108460 Drosophil
39		46.8	2.9	932	122	CNS0072Q	AL066742 Drosophil
C 40		46.2	2.8	477	64	AW134706	AW134706 UT-H-Bil-
C 41		46.2	2.8	477	64	AW134707	AW134707 UT-H-Bil-
42		45.6	2.8	361	89	T28073	T28073 EST26562 Hu
43		44	2.7	446	27	AA495728	AA495728 zw04a09.r
44		43.6	2.7	910	122	CNS006ON	AL065629 Drosophil
C 45		43.2	2.7	776	122	CNS010RY	AL099352 Drosophil

ALIGNMENTS

RESULT 1
AW630744 517 bp mRNA EST 31-MAR-2000
LOCUS hb87a03.y1 NCI-GAP.GUL Homo sapiens cDNA clone IMAGE:2969740 5'
DEFINITION similar to gb:X04430 INTERLEUKIN-6 PRECURSOR (HUMAN);, mRNA

sequence.
AW630744
VERSION AW630744.1 GI:7377534
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 517)
AUTHORS NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 6, 2000 this sequence version replaced gi:6676648.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov

Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center

Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 422.

FEATURES
Location/Qualifiers
1..517
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2969740"
/clone_lib="NCI-GAP.GUL"
/tissue_type="2 pooled high-grade transitional cell tumors"
/lab_host="DH10B"
/note="Organ: genitourinary tract; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies."

BASE COUNT 149 a 139 c 123 g 106 t
ORIGIN
Query Match 23.4%; Score 380; DB 79; Length 517;
Best Local Similarity 98.7%; Pred. No. 8.4e-89;
Matches 383; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1057 ccagttacccccaggagaagattcccaaatgttagcgccccacacagacagccactcacc 1116
Db 130 CCAGTACCCCGGAGAGAGATTCCAAAGATGTAGCGCGCCACACAGACAGCCACTCACC 189
Qy 1117 tcttcagaacgaattgacaaacaaattcggtacatcctcgacgcatctcagccctgaga 1176
Db 190 TCTTCAGAACGAATTGACAAACAAATTCGGTACATCTCTCGAGCGGATCTCAGCCCTGAGA 249
Qy 1177 aaggagacatgttaacaagagtaacatgtgtgaaacagacaaagagcactgcagaaaaac 1236
Db 250 AAGGAGACATGTAAACAGAGTAACATGTGTGAAGCAGCAAGAGAGGCGACTGCGCAGAAAAC 309
Qy 1237 aacctgaacctcccaaatgaggtggtgaaataatgagatccttcacatctggattcaatgag 1296
Db 310 AACCTGAACCTTCCAAAGATGCTGAAAAGATGATGCTTCCAAATCTGGATTCAATGAG 369
Qy 1297 gagacttccctgggtaaaatcatcactggtcttttggagtttgaggtatcactagatgac 1356
Db 370 GAGACTTCCCTGGTGAAATCATCACTGGTCTTTTGGAGTTTGGAGGTATACCTAGAGTAC 429
Qy 1357 ctccgaacagatttgagtagtgaggagaaacaaagccagagctgtgcagatgagttacaaa 1416
Db 430 CTCACAGACAGATTGACAGTAGTAGTGCAGGAACAGCCAGAGCTGTGCACATGAGTACAAA 489
Qy 1417 gtctgtatccagtttctcctgcagaaaaaagg 1444

QY	1177	aaggagacatgttaacaagagtgtaacatgtgtgaagacagcaagagggcaactggcagaaac	1231
Db	264	AAGGAGACATGTAAACAGAGTAAACATGTGTGAAGACGCAAGAGGCACTGGCAGAAAC	323
QY	1237	aagctgaacctccaagatggct-gaaaaagatgagatgcttccaatctggattcaatga	1295
Db	324	AACCTGACCTTCCAAGATGGCTCGAANAAGATGGATGCTTCCANNCTGGATTCAATGA	383
QY	1296	ggagacttgcctggtgtaaaatcatcac-tgggtcttttggagtttgaggtatcacctagagt	1354
Db	384	GGAGACTTGCCTGGTCAAAATCATCACTTGGTCTTTTGGAGTTTGAGGTATACCTAGAGT	443
QY	1355	acctcagaacagatttgagtag-tgaggaacagccagagctgtgcagatgagtaca	1413
Db	444	ACCTCCAGACACAGATTTGAGTAGTGTGAGGAACCAAGCCAGAGCTGTGCAGATGAGTACA	503
QY	1414	aaagtctgatccagttctctgcagaaaaagcgaagaatctagatgcaataaccacccc-	1472
Db	504	AAGTCTGTATCCAGTTCCTTGTGAGAAAAAGGCNAAGAAATCTAGATGCNATNACCACCCCT	563
QY	1473	tgaccccaaccacaaatgccagctgctgcagca	1504
Db	564	TGACCCCAACCAATGCCAGCCTGCTGACGA	595
RESULT 3			
AI751501			
LOCUS	AI751501	481 bp	mRNA
DEFINITION	cn10c12.y1	Normal Human Trabecular Bone Cells	EST 22-JUN-1999
ACCESSION	clone NHTBC_cni0c12	random, mRNA sequence.	
VERSION	AI751501		
KEYWORDS	AI751501.1	GI:5129765	
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	1 (bases 1 to 481)		
	Jia, L.B., Young, M.F., Touchman, J.W., Bouffard, G.G., Beckstrom-Sternberg, S.M., Green, E.D., Powell, J.I., Yang, L.M., Robey, P.G., Hotchkiss, R.N. and Francomano, C.A.		
TITLE	Scap: The Skeletal Genome Anatomy Project		
JOURNAL	Unpublished (1997)		
COMMENT	On Jun 22, 1998 this sequence version replaced gi:3247051.		
	Contact: Libin Jia		
	Medical Genetics Branch		
	National Human Genome Research Institute		
	10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA		
	Tel: 301-402-4877		
	Fax: 301-496-7157		
	Email: libin@helix.nih.gov		
	DNA Sequencing and analyses by National Institutes of Health		
	Intramural Sequencing Center (NISC).		
	Plate: 10 row: c column: 12		
	Seq primer: M13RP1 reverse primer (ABI).		
FEATURES	Location/Qualifiers		
source	1..481		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="NHTBC_cni0c12"		
	/clone_lib="Normal Human Trabecular Bone Cells"		
	/sex="Female"		
	/tissue_type="Bone"		
	/cell_type="Trabecular Bone Cells"		
	/lab_host="SURE"		
	/note="Organ: Hip; Vector: pBluescript; Site_1: EcoRI"		
BASE COUNT	137 a 131 c 112 g 101 t		
ORIGIN			
Query Match	22.4%	Score 364;	DB 43; Length 481;
Best Local Similarity	100.0%	Pred. No. 1.3e-84;	
Matches 364;	Conservative	0; Mismatches	0; Indels 0; Gaps

/clone_lib="Soares_senescent_fibroblasts_NBHSF"
/tissue_type="senescent_fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: p7T3D (Pharmacia) with a modified
polylinker V_TYBE: phagemid; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5']
TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3',
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7T3D vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo."
Soares a 143 c 123 g 231 t 1 others

Query Match 17.5%; Score 286.4; DB 35; Length 731;
Best Local Similarity 94.5%; Pred. No. 2.6e-64;
Matches 307; Conservative 0; Mismatches 17; Indels 1; Gaps 1;
QY 1303 tgcctgtgaaatcatcactgctcttttggagtttgagttatcacctagtagtacctccag 1362
Db 731 TGCNTGTTGAAATCATCACTGCTCTTTTGGAGTTTGGAGTATCACTAGAGTACTTCAAG 672
QY 1363 aacagatttgagtagtgaggaacagccagagctgtgcagatgagtagtacaagaagctc-t 1421
Db 671 ACCAGATTTTCAGAGTAGTGAGGACACAGCCAAAGCTGTGCAGATGAGTACAAAGTCTT 612
QY 1422 gatccagttctgcagaaaaagggcaagaatctagatgcaataaccacccctgacccaac 1481
Db 611 GATCCAGTTCTTCAGAAAAAGGCAAGAATCTAGATGCAATACCAACCCTGACCCCAAC 552
QY 1482 cacaaatgcagcctgtgcagagctgcagagtcgagggcacagaaacagtgctgcagacatgac 1541
Db 551 CACAAATGCCAGCCTGTCTGACGAGCTGTCAGGACAGACAGACAGTGGCTGCAGGACATGAC 492
QY 1542 aactcatctcttcgcagcagcttgaagaggttcctgcagtcacagcctgagggctcttcg 1601
Db 491 AACTCATCTCATTTCTGCGCAGCTTTTAAAGGAGTTCCTGCAGTCCAGCCTGAGGGCTCTTCG 432
QY 1602 gcaaatgtagcagggcaccgtcga 1626
Db 431 GCAAAATGATGATGGCACCTCAGA 407

RESULT 6
AI824041/c
LOCUS
DEFINITION
w129h07.x1 NCI-CGAP_kid12 Homo sapiens cDNA clone IMAGE:2404285 3'
similar to gb:X04430 INTERLEUKIN-6 PRECURSOR (HUMAN);, mRNA
sequence.
AI824041
AI824041.1 GI:5444712
VERSION
KEYWORDS
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 725)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bhrp/image/image.html
Insert length: 1194 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 450.
Location/Qualifiers
source
1..725
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2404285"
/clone_lib="NCI-CGAP_kid12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/note="Organ: kidney; Vector: p7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI-CGAP_kid5 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1323912-1325831, 1471368-1472903 and
1492104-1493255). Subtraction by Bento Soares and M.
Fatima Bonaldo."
Soares a 142 c 125 g 226 t

Query Match 17.3%; Score 281; DB 44; Length 725;
Best Local Similarity 96.3%; Pred. No. 6.8e-63;
Matches 309; Conservative 0; Mismatches 10; Indels 2; Gaps 2;
QY 1306 ctggtgaaatcatcactgctcttttggagtttgagttatcacctagtagtacctccagaac 1365
Db 725 CTGTCGAAATCAATCA- TGTCTTTTGAAGTTTGAAGTATACCTAGAGTA-CTCCAGCAC 668
QY 1366 agatttgagtagtgaggaacagccagagctgtgcagatgagtagtacaagaagctctgac 1425
Db 567 AGATTTGAGAGTAGTGAGGACACAGCCAGATCTGTGCAGATGAGTACAAAGTCTCTGATC 608
QY 1426 cagtctctgcagaaaaagggcaagaatctagatgcaataaccacccctgacccaaccaca 1485
Db 607 CAGTTCTCTCAGAAATAGGCAAGAAATCTAGATGCAATACCAACCCTGACCCCAACCACT 548
QY 1486 aatgcagcctgtgcagagctgcagggcacagaaacagtgctgcagggacatgacaact 1545
Db 547 AATGCCAGCCTGCTGACGAAAGCTGCAGGCACAGAACAGTGGCTGCAGGACATGACAACT 488
QY 1546 catctcattctgcagcagcttgaagaggttcctgcagtcacagcctgagggctcttcgcaa 1605
Db 487 CATCTCATTTCTGCGCAGCTTTAAGGAGTTCCTGCAGTCCAGCCTGAGGGCTCTTTCGGCAA 428
QY 1606 atgtagcagtgggcaccgtcga 1626
Db 427 ATGTAGCATGGCACCTCAGA 407

RESULT 7
T29234
LOCUS
DEFINITION
EST73852 Human Bone Homo sapiens cDNA 5' end similar to interleukin
6 (H7:1314), mRNA sequence.
ACCESSION
T29234
VERSION
T29234.1 GI:611332
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 287)
ADAMS,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,

Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghegan, N.S.M., Glodok, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinklejr, P.S., Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudak, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, J.C., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 83 Million Basepairs of cDNA Sequence
Nature 377, 3-174 (1995)

JOURNAL
MEDLINE
COMMENT

On Dec 20, 1995 this sequence version replaced gi:1135864.

Contact: Venter, JC

The Institute for Genomic Research

932 Clopper Rd, Gaithersburg, MD 20878

Tel: 3018699056

Fax: 3018699423

Email: tdbinfo@db.tigr.org

For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@db.tigr.org).

Insert Length: 716 Std Error: 0.00

Seq primer: M13 Reverse

High quality sequence stop: 92.

Location/Qualifiers

1. 287

/organism="Homo sapiens"

/db_xref="ATCC (inhost):105671"

/db_xref="taxon:9606"

/clone.lib="Human Bone"

/tissue.type="bone"

BASE COUNT 81 a 69 c 68 g 65 t 4 others

ORIGIN

Query Match 15.3%; Score 248.6; DB 89; Length 287;
Best Local Similarity 96.9%; Pred. No. 1.6e-54;
Matches 251; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1368 atttgaagtagtgaggacaagccagagctgtgcagatgacatacaaaagtcctgattcca 1427

Db 1 ATTTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGATGACAAANTCCTGATCCA 60

QY 1428 gtctctgcagaaaaggcaagaattctagatgcaataaccacccctgaccccaaccacaaa 1487

Db 61 NTTCCTGCAGAAAGGCAAGCAANTCTAGATGCAATAACCACCCCTGACCCCAACCAAAA 120

QY 1488 tgcagcctctgtcagagctgcagggacagaaaccagtgctgcaggagacatacaactca 1547

Db 121 TGCCAGCNTGCTGACGAAGCTGCAGGCACAGAACCAAGTGGCTGCAGGACATGACAACCTCA 180

QY 1548 tctcattctgcagctttaagagattctctgcagtcacagctgagccttcttcggcaaat 1607

Db 181 TCTCATTTGCGCAGTTTTTAAGGAGTTCTCTGCAGTCCAGCCTTGAGGGCTCTTCGGCAANT 240

QY 1608 gtacgatggcaccgtcga 1626

Db 241 GTAGCATGGCACCCTCAGA 259

RESULT 8

AI472218/c

LOCUS

DEFINITION

tj86e02.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148410 3' similar to gb:X04430 INTERLEUKIN-6 PRECURSOR (HUMAN);, mRNA sequence.

AI472218 655 bp mRNA EST 14-APR-1999

tj86e02.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone

IMAGE:2148410 3' similar to gb:X04430 INTERLEUKIN-6 PRECURSOR

(HUMAN);, mRNA sequence.

ACCESSION

VERSION AI472218.1 GI:4334308

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 655)

NCT-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

TITLE Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT On May 18, 1998 this sequence version replaced gi:3138589.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 709 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 444.

FEATURES

source

1. 655

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone.lib="Soares NSF_F8_9W_OT_PA_P_S1"

/lab.host="DH10B"

/note="Organ: pooled; Vector: pT7M3D-Pac (Pharmacia) with

a modified polylinker; Site_1: Not 1; Site_2: Eco RI;

Equal amounts of plasmid DNA from five normalized

libraries were mixed, and ss circles were made in vitro.

Following HAP purification, this DNA was used as tracer in

a subtractive hybridization reaction. The driver was

PCR-amplified cDNAs from pools of 5,000 clones made from

the same 5 libraries. The pools consisted of the following

libraries and clones: Soares NBHSF pool 1:

309384-310919, 323208-325895 Soares ND2HP pool 1:

145032-147335, 147720-148103, 148872-149255, 15002 -

150407, 151176-152327 Soares NB2HF8-9W pool 1:

758280-760583, 772104-774407 Soares NBHPA pool 1:

304776-306311, 320136-322823, 326280-326663 Soares NBHOT

pool 1: 723720-726407, 739080-740999 Subtraction by Bento

Soares and M. Fatima Bonaldo."

BASE COUNT 201 a 125 c 113 g 213 t 3 others

ORIGIN

Query Match 14.8%; Score 240.2; DB 40; Length 655;

Best Local Similarity 97.6%; Pred. No. 3e-52;

Matches 242; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1379 qtgaggaacaagccagagctgtgcagatgacatacaaaagtcctgattccctgcaga 1438

Db 655 GTGAGGANCAGCCAGAGCTGTGCAGATGATGACAAAGTCTGTGATCCAGTTCCTGCAGA 596

QY 1439 aaaaagcaagaatactagatgcaataaccacccctgaccccaaccacaatgccagcctgc 1498

Db 595 AAAAGGCAAGAATCTAGATGCAATAACCCCTGACCCCAACCAACNAATGCCAGCCTGC 536

QY 1499 tgaagaagctgcaggacagaaaccagtggtgcaggacatgacaactcatctctgc 1558

Db 535 TCACGAAGCTGCAGGCACAGAACCCAGTGGCTGCAGGACATGACAACTCATCTCATTTCTGC 476

QY 1559 gcagctttaagagattctctgcagtcacagccttcctgcgcaaatgtagcatggc 1618

Db 475 GCAGCTTTAAGGAGTTCTCTGCAGTCCAGCTCGAGGGCTCTTCGGCAATGATGCGC 416

QY 1619 accgtcga 1626

Db 415 ACCTCAGA 408

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Qy 1467 caccctgacccaaacacaaatgccagctgctgacgaagctgcaggccacagaacacgtg 1526
|||||
Db 73 CACCCTGACCCACACCAAAATGCCAGCTGCTGACGAAGCTGCAGGACACAGAACCACTG 132
|||||
Qy 1527 gctcagagacatgacaactcatctctatctctgacgagcttttaaggagttcctcgcagtcacg 1586
|||||
Db 133 GCTCAGAGACATGACAACATCATCTCATCTCGCGCANTTTAAAGGAGTTCCTGCGAGTCCAG 192
|||||
Qy 1587 cctgaggctcttcgcaaatgtagctggcagccactgcga 1626
|||||
Db 193 CTTGAGGCTCTTCGGCAATGTAGCATGGCAGCCACTCAGA 232
|||||

RESULT 11
AA381892 311 bp mRNA EST 21-APR-1997
LOCUS AA381892
DEFINITION EST95205 Activated T-cells 1 Homo sapiens cDNA 5' end similar to
interleukin 6, mRNA sequence.
ACCESSION AA381892
VERSION AA381892.1 GI:2034376
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 311)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
12140200
Other_ESTs: THC167228
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
1. .316
/organism="Homo sapiens"
/db_xref="ATCC (inhost):186438"
/db_xref="taxon:9606"
/clone_lib="Activated T-cells I"
/cell_type="T-lymphocyte"
/dev_stage="adult"
/note="vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 86 a 99 c 68 g 58 t
ORIGIN

```

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Query Match 11.4%; Score 186; DB 25; Length 311;
Best Local Similarity 100.0%; Pred. No. 3.6e-38;
Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1057 ccagtacccccagagagaagattccaaaatgttagcgcgcacacacagacagccactcacc 1116
|||||
Db 126 CCAGTACCCCGGAGAGATTCCAAAGATGTAGCGCGCCACACAGACAGCACTCACC 185
|||||
Qy 1117 tcttcagacaattgacaaaattcggtacatctctcagcgcacatctcagccctgaga 1176
|||||
Db 186 TCTTCAGAACGAATTGACAAACAATTCGGTACATCTCGAGCGCATCTCAGCCCTGAGA 245
|||||
Qy 1177 aaggagacatgtaacaagtagtaacatgtgtgaaacagcaagaagcgcactgcgcaaaaac 1236
|||||
Db 246 AAGGAGACATGTAAACAGATTAACATGTGTGAACAGCAAGAGGCACTGGCAGAAAAC 305
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Qy 1237 aacctg 1242
|||||
Db 306 AACCTG 311

RESULT 12
AA380919 316 bp mRNA EST 21-APR-1997
LOCUS AA380919
DEFINITION EST93950 Activated T-cells V Homo sapiens cDNA 5' end similar to
interleukin 6, mRNA sequence.
ACCESSION AA380919
VERSION AA380919.1 GI:2033259
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 316)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
12140200
Other_ESTs: THC167228
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
1. .316
/organism="Homo sapiens"
/db_xref="ATCC (inhost):185336"
/db_xref="taxon:9606"
/clone_lib="Activated T-cells V"

FEATURES
source

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/cell_type="T-lymphocyte"
/dev_stage="adult"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      82 a 103 c 72 g 58 t 1 others
ORIGIN

Query Match      10.6%; Score 172.4; DB 25; Length 316;
Best Local Similarity 98.9%; Pred. No. 1.3e-34;
Matches 173; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1057 ccagtagcccccagagaagattccaaagatgtagcgcgcacacagacagccactcacc 1116
Db 142 CCAGTACCCCCAGGAGAAGATTCCAAAGATGTAGCCGCCCCACACAGACAGCCACTCACC 201
QY 1117 tcttcagacgaattgacaaacaaattcggtacatctctcagcgcctcagccctgaga 1176
Db 202 TCTTCAGACGAATTGACAAACAAATTCGGTACATNCTCGACGGCATCTCAGCCCTGAGA 261
QY 1177 aaggagacatgtacaagagtaacatgtgtgaagcagcagaagaggcactggcag 1231
Db 262 AAGGAGACATGTACAGAGTACATGTGTAAAGCAGCAAGAGGCATCGGCAG 316

RESULT 13
AI343270/c
LOCUS      AI343270      594 bp      mRNA      EST      18-MAR-1999
DEFINITION tb94c07.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:2061996 3'
            similar to gb:X04430 INTERLEUKIN-6 PRECURSOR (HUMAN);, mRNA
            sequence.
ACCESSION  AI343270
VERSION     AI343270.1 GI:4080476
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 594)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
            M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/Dbrrp/image/image.html
            Insert Length: 823 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 473.
FEATURES
            Location/Qualifiers
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                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:2061996"
                /clone_lib="NCI_CGAP_Col6"
                /tissue_type="colon tumor, RER+"
                /lab_host="DH10B"
                /note="Organ: colon; Vector: pT73B-Pac (Pharmacia) with a
                modified polylinker; Site_1: Not I; Site_2: Eco RI;
                Plasmid DNA from the normalized library NCI_CGAP.Col6 was
                prepared, and ss circles were made in vitro. Following HAP
                purification, this DNA was used as tracer in a subtractive
                hybridization reaction. The driver was PCR-amplified cDNAs
                from a pool of 5,000 clones made from the same library
                (cloneIDs 1057416-1061255, and 1144584-1145351).

```

```

Subtraction by Bento Soares and M. Fatima Bonaldo.
BASE COUNT      197 a 109 c 100 g 188 t
ORIGIN

Query Match      10.4%; Score 169.2; DB 38; Length 594;
Best Local Similarity 97.8%; Pred. No. 1.1e-33;
Matches 182; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1442 aggcagaagaatctagatgcaat-aaccacccctgaccacacacaaatgccagctgctg 1500
Db 594 AGGCAAGAATCTAGATGCAATAAACCCCTGACCCCAACACCAAAATGCCAGCTGCTGTG 535
QY 1501 acgaagctcgaggcacagaacacagtgctgcagacatgacaactcatctctgcgc 1560
Db 534 ACGNAGTGGACGACAGAACCACTGCTGCAGGACATGACAACTCATCTCTCTCTGGCC 475
QY 1561 agctttaagagtgcttcgagtcagtcagcctgagggctcttcggcaaatgtagcggcac 1620
Db 474 AGCTTTAAGAGTTCCTGCAGTCCAGCTCAGGGCTCTTCGGCAAATGTAGCATGGGCAC 415
QY 1621 cgtcga 1626
Db 414 CTCAGA 409

RESULT 14
AW630409
LOCUS      AW630409      311 bp      mRNA      EST      31-MAR-2000
DEFINITION hh76g07.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968764 5'
            similar to gb:X04430 INTERLEUKIN-6 PRECURSOR (HUMAN); contains
            PTR5.b1 PTR5 repetitive element ;, mRNA sequence.
ACCESSION  AW630409
VERSION     AW630409.1 GI:7377199
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 311)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
            Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
            I.M.A.G.E. Consortium DNA Sequencing by: Washington University
            Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            image.llnl.gov/image/html/iresources.shtml
            Seq primer: -40RP from Gibco
            High quality sequence stop: 213.
FEATURES
            Location/Qualifiers
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                /db_xref="taxon:9606"
                /clone="IMAGE:2968764"
                /clone_lib="NCI_CGAP_GU1"
                /tissue_type="2 pooled high-grade transitional cell
                tumors"
                /lab_host="DH10B"
                /note="Organ: genitourinary tract; Vector: pCMV-SPORT6;
                Site_1: SalI; Site_2: NotI; Cloned unidirectionally.
                Primer: Oligo.dT. Library constructed by Life
                Technologies."
BASE COUNT      76 a 96 c 77 g 60 t 2 others
ORIGIN

```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: August 8, 2000, 23:47:59 ; Search time 65.69 Seconds
(without alignments)
3406.962 Million cell updates/sec

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Title: US-09-142-471-1
Perfect score: 1627
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 243080 seqs, 68777915 residues

Total number of hits satisfying chosen parameters: 486160

Minimum	DB	seq	length:	0
Maximum	DB	seq	length:	10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: /cgn2_6/ptodata/2/ins/backfiles1.seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	995	61.2	2061	7	5171840-1	Patent No. 5171840
2	995	61.2	2061	7	5480796-1	Patent No. 5480796
3	969	59.6	1074	3	US-08-627-151A-15	Sequence 15, Appl
4	969	59.6	1404	7	5171840-8	Patent No. 5171840
5	969	59.6	1404	7	5480796-8	Patent No. 5480796
6	563.6	34.6	1145	7	5510472-1	Patent No. 5510472
7	551.8	33.9	555	1	US-08-437-680A-1	Sequence 1, Appl
8	550.4	33.8	561	1	US-07-745-382-19	Sequence 19, Appl
9	550.4	33.8	561	1	US-07-921-848-19	Sequence 19, Appl
10	550.4	33.8	561	1	US-08-165-301A-19	Sequence 19, Appl
11	550.4	33.8	561	6	PCR-US94-14179-19	Sequence 19, Appl
12	539.2	33.1	951	5	US-08-469-313-57	Sequence 57, Appl
13	539.2	33.1	951	6	PCR-US95-01185-57	Sequence 57, Appl
14	538.4	33.1	540	6	PCR-US94-12873-3	Sequence 3, Appl
15	535.8	32.9	555	2	US-08-567-047-1	Sequence 3, Appl
16	535.8	32.9	555	3	US-08-567-048-1	Sequence 1, Appl
17	531.2	32.6	561	5	US-08-469-318-175	Sequence 1, Appl
18	531.2	32.6	561	6	PCR-US95-01185-175	Sequence 175, App
19	529.4	32.5	555	3	US-08-693-182-1	Sequence 175, App
20	529.4	32.5	555	4	US-09-008-482-1	Sequence 1, Appl
21	526.2	32.3	555	4	US-08-945-529-1	Sequence 1, Appl
22	526.2	32.3	555	4	US-08-945-529-4	Sequence 4, Appl
23	526.2	32.3	555	4	US-08-945-529-5	Sequence 5, Appl
24	526.2	32.3	555	4	US-08-945-529-6	Sequence 6, Appl
25	525	30.2	525	1	US-08-009-973-2	Sequence 2, Appl
26	491	30.2	555	4	US-08-945-529-7	Sequence 7, Appl

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RESULT 1
5171840-1
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:1:
; LENGTH: 2061
5171840-1

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ALIGNMENTS

Query Match	61.2%;	Score 995;	DB 7;	Length 2061;
Best Local Similarity	100.0%;	Pred. No. 1.6e-237;		
Matches 995;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	8	catggagtgtagccgaggaggaacatgctgcgcgtcgactcgcgcctctgactgcc	67	
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QY	68	tgtctggccgcgcgggagcgcgtgcgtccccaaagcgcctgcctgcagagagtgca	127	
Db	281	tgtctggccgcgcgggagcgcgtgcgtccccaaagcgcctgcctgcagagagtgca	340	
QY	128	gaggcgtgctgaccagtcctgccaggagaacagctgactctgaacctgccgggggtaga	187	
Db	341	gaggcgtgctgaccagtcctgccaggagaacagctgactctgaacctgccgggggtaga	400	
QY	188	cgaagaacaatgccacttgttcaactggctgcaggaaagccggctgcaggctcccaccca	247	
Db	401	cgaagaacaatgccacttgttcaactggctgcaggaaagccggctgcaggctcccaccca	460	
QY	248	gcagatgggctggcatgggaaggaggtgctgctgaggctcggtgcagctccacgactcg	307	
Db	461	gcagatgggctggcatgggaaggaggtgctgctgaggctcggtgcagctccacgactcg	520	
QY	308	gaaactattcatgtataccggggccgcgcagctgggactgtgcaacttgtgtgatg	367	
Db	521	gaaactattcatgtataccggggccgcgcagctgggactgtgcaacttgtgtgatg	580	
QY	368	ttccccccgaggagccacagctctcctgcttccggaaagacccctcagcaaatgtgtt	427	
Db	581	ttccccccgaggagccacagctctcctgcttccggaaagacccctcagcaaatgtgtt	640	
QY	428	gtgagtggggtctctcgagcaccccatctcttgacgacaaaaggtctgtcttgtgagga	487	

[illegible]

```

Query Watch      59.6%; Score 969; DB 7; Length 1404;
best Local Similarity 100.0%; Pred. No. 3.9e-231;
Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 atgtggcagtgatgcagctactgctgctctgtgcccgcgcggagcggcgctg 93
|||||
Db 1 atctggcctgcggctggcgtgctgctgctgctgcccgcgcggagcggcgctg 60
|||||

04 caccacacacagctgacctccacacacagctgacacagagcctgctgaccactctgcacaga 153

```


Db 421 CCACCAACCAATGCCGCTGCTGACCAAGCTGCAGSCACAGAACCAAGTGGCTGCAGGAC 480
QY 1537 atgacaactcatctatctgcgcagctttaagaggtctctgcagtcacagccttgaggct 1596
Db 481 ATGCAACTCATCTCATCTCTCGGAGCTTTAAGGAGTTCTGCAGTCCAGCCTGAGGGCT 540
QY 1597 cttcgcaaatgtag 1611
Db 541 CTTGGCAAAATGTAG 555

RESULT 8

US-07-745-382-19
; Sequence 19, Application US/07745382
; Patent No. 5270181
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: Lavallie, Edward
; TITLE OF INVENTION: Peptide and Protein Fusions To
; TITLE OF INVENTION: Thioedoxin and Thioedoxin-Like Molecules
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/745.382
; FILING DATE: 19910814
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/652,531
; FILING DATE: 06-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseri, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: G5188A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..558
US-07-745-382-19

Query Match 33.8%; Score 550.4; DB 1; Length 561;
Best Local Similarity 98.9%; Pred. No. 1.3e-127;
Matches 554; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1052 tcagcagccagtcacccagagagatcccaagatgtagccgccccacacagacagccac 1111
Db 2 TGCGTCCAGTACCTCCAGGTGAGATTCCTAAGATGTAGCGCCGCCACACAGACGCCAC 61
QY 1112 tcacctttcagaacgaattgacaaataattcggtacatactcagcggcatctcagccc 1171
Db 62 TCACCTCTTCAGAACGAATTGACAAATAATTCGGTACATCTCTCGAGCGCATCTCAGCCC 121

QY 1172 tgagaagagagacatgtacaagagtagtaacatgtgtgaaagcagcaagaggcactggcag 1231
Db 122 TGAGAAGAGAGACATGTAACAAGAGTAACATGTGTGAAAGCAGCAAAAGAGGACTGGCAG 181
QY 1232 aaaaacacctgaaccttccaaagatggtgaaaaagatggtgcttcccaatctggaattca 1291
Db 182 AAAACAACTGAAACCTTCCAAAGATGGCTGAAAAAGATGGATGCTTCCAACTCTGGATTCA 241
QY 1292 atgagagagacttgctggtgaaataatcactcgtgtcttttgaggttgagggtataacctag 1351
Db 242 ATGAGGAGACTTGGCTGGTGAAAAATCATCACTGCTCTCTTTTGGAGTTGAGGTATACCTAG 301
QY 1352 agtacctcagaacagatttgagtagtagtagagagagacaaagcagcagctgtgcagatagta 1411
Db 302 AGTACCTCCAGAACAGATTGAGAGTAGTAGGAGAACAGCAGAGCTGTGCAGATGAGTA 361
QY 1412 caaaagctcgtatccagttcctgcagaaaaagcgaagaatctagatgcaataaccacc 1471
Db 362 CAAAAGTCTGTATCCAGTTCCTGCAGAAAAAGCAAGAAATCTAGATGCAATAACCAACC 421
QY 1472 ctgacccaacacaaatgcccagcctgctgcagagctgcagagcttaagaggttccctgcagctcag 1531
Db 422 CTGACCCCAACCAAAATGCCAGCTGCTGACGAAGCTGCAGGACAGAACCAAGTGGCTGC 481
QY 1532 agacatgacaactcatctcatctctctcgcagcttgcagcttaagaggttccctgcagctcag 1591
Db 482 AGGACATGACAATCTATCTCTCTGCGCAGCTTTAAGGAGTTCCTGCTCAGTCCAGCCTGA 541
QY 1592 gggctcttcggcaaatgtag 1611
Db 542 GGGCTCTTCGGCAAAATGTAG 561

RESULT 9

US-07-921-848-19
; Sequence 19, Application US/07921848
; Patent No. 5292646
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: Lavallie, Edward
; TITLE OF INVENTION: Peptide and Protein Fusions To
; TITLE OF INVENTION: Thioedoxin and Thioedoxin-Like Molecules
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/921.848
; FILING DATE: 19920728
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/652,531
; FILING DATE: 06-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,382
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseri, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: G5188A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..558
US-07-921-848-19

Query Match 33.8%; Score 550.4; DB 1; Length 561;
Best Local Similarity 98.9%; Pred. No. 1.3e-127;
Matches 554; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1052 tcgagccagatccccagagagagattccaaagatgtacccgccccacacagacagccac 1111
Db 2 TGCGTCCAGTACTCCAGGTGAAGATTCTAAAGATGTAGCGCCGCCACACAGACGCCAC 61

QY 1112 tcacctctcagaacgaattgacaaattcggtacatcctcgacgcatctcagccc 1171
Db 62 TCACCTCTTCAGAACGAATTGACAAACAATTCGGTACATCTCGACGGCATCTCAGCCC 121

QY 1172 tgagaagagacatgtacaagagtaacatgtgtgaaagcagcaagagcactggcag 1231
Db 122 TGAGAAAGGAGACATGTACAAGAGTAACATGTGTGAAAGCAGCAAGAGGCACCTGCGCAG 181

QY 1232 aaacaacacctgaaccttccaaagatgctgaaagagtgatgcttccaaatcggattca 1291
Db 182 AAAACAACCTGAACCTTCCAAAGATGGCTGAAAGATGGATGCTTCCAATCTGGATTCA 241

QY 1292 atgaggaacttgcctgggaaataatcaatcggtcttttgagtttgaggtatacctag 1351
Db 242 ATGAGGAGACTTGCCTGGTGAATAATCATCTGCTTTTGGAGTTTGAGGTATACCTAG 301

QY 1352 agtacctccagaacagatttgagagtagtgaggaacaagccagagctgtgcagatgagta 1411
Db 302 AGTACCTCCAGAACAGATTGTAGAGTAGTGAAGAAAGCAAGAAATCTAGATGCAATAACCCACC 421

QY 1412 caaaagtctgtatccagcttccaaagatgctgaaagagtgatgcttccaaatcggattca 1471
Db 482 AGGACATGACAACTCATCTCTTCGCGCAGCTTTAAGGAGTTCCTGCGAGTCCAGCCTGA 541

QY 1592 gggctcttcggcaaatgtag 1611
Db 542 GGGCTCTTCGGCAAAATGTAG 561

RESULT 10
US-08-165-301A-19
Sequence 19, Application US/08165301A
Patent No. 5646016
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallie, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive

CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,301A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meinert, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..558
US-08-165-301A-19

Query Match 33.8%; Score 550.4; DB 1; Length 561;
Best Local Similarity 98.9%; Pred. No. 1.3e-127;
Matches 554; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1052 tcgagccagatccccagagagagattccaaagatgtacccgccccacacagacagccac 1111
Db 2 TGCGTCCAGTACTCCAGGTGAAGATTCTAAAGATGTAGCGCCGCCACACAGACGCCAC 61

QY 1112 tcacctctcagaacgaattgacaaattcggtacatcctcgacgcatctcagccc 1171
Db 62 TCACCTCTTCAGAACGAATTGACAAACAATTCGGTACATCTCGACGGCATCTCAGCCC 121

QY 1172 tgagaagagacatgtacaagagtaacatgtgtgaaagcagcaagagcactggcag 1231
Db 122 TGAGAAAGGAGACATGTACAAGAGTAACATGTGTGAAAGCAGCAAGAGGCACCTGCGCAG 181

QY 1232 aaacaacacctgaaccttccaaagatgctgaaagagtgatgcttccaaatcggattca 1291
Db 182 AAAACAACCTGAACCTTCCAAAGATGGCTGAAAGATGGATGCTTCCAATCTGGATTCA 241

QY 1292 atgaggaacttgcctgggaaataatcaatcggtcttttgagtttgaggtatacctag 1351
Db 242 ATGAGGAGACTTGCCTGGTGAATAATCATCTGCTTTTGGAGTTTGAGGTATACCTAG 301

QY 1352 agtacctccagaacagatttgagagtagtgaggaacaagccagagctgtgcagatgagta 1411
Db 302 AGTACCTCCAGAACAGATTGTAGAGTAGTGAAGAAAGCAAGAAATCTAGATGCAATAACCCACC 361

QY 1412 caaaagtctgtatccagcttccaaagatgctgaaagagtgatgcttccaaatcggattca 1471
Db 362 CAAAAGTCTCTGATCCAGTTCCTCGAGAAAGGCAAGAAATCTAGATGCAATAACCCACC 421

QY 1472 ctgaccacaacacaaatgccagctgctgacgaagctgcagggcacagacacagtggtgc 1531
Db 422 CTGACCCCAACCAACAATGCCAGCTGCTGACGAGAGCTGCGAGGCACACAAACCATGGCTGC 481

QY 1532 aggacatgacaactcatctcattctgcgcagctttaaggagtttctcagctccagcctga 1591
Db 482 AGGACATGACAACTCATCTCTTCGCGCAGCTTTAAGGAGTTCCTGCGAGTCCAGCCTGA 541

Qy 1592 gggtctctcggaatgtag 1611
 |||||
Db 542 GGGCTCTTCGGCAATGTAG 561

RESULT 11

PCT-US94-14179-19
: Sequence 19, Application PC/TUS94/14179
: GENERAL INFORMATION:
: APPLICANT: McCoy, John
: APPLICANT: DiBlasio-Smith, Elizabeth
: APPLICANT: Grant, Kathleen
: APPLICANT: Lavallie, Edward R.
: TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
: TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
: TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc.
: STREET: 87 CambridgePark Drive
: CITY: Cambridge
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/14179
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Meinert, M. C.
: REGISTRATION NUMBER: 33,544
: REFERENCE/DOCKET NUMBER: GI 5188D
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 876-1170
: TELEFAX: (617) 876-5851
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 561 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: unknown
: MOLECULE TYPE: DNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..558
PCT-US94-14179-19

Query Match 33.8%; Score 550.4; DB 6; Length 561;
Best Local Similarity 98.9%; Pred. No. 1.3e-127;
Matches 554: Conservative 0; Mismatches 6; Indels 0

Qy	1052	tcgagccagtaacc	ccccccaggagaa	gattccaa	agatgtagccgc	ccccacacagacagccac	1111
Db	2	TGGCTCCAGTACCT	TCCAGGTCGAAGATTCT	TAAGATGTAGCG	CGCCACACAGACAGGCAC		61
Qy	1112	tcaccttcgaaacga	tigacaaacaa	aattcggta	ctactctcgacg	catctcagccc	1171
Db	62	TCACCTCTTCAGAC	GAAATTCACAA	CAAAATTCGGTACATCCT	CGACGGCATCTCAGGCC		121
Qy	1172	tgagaaaggagacatg	taacaaagagta	acaatgtgtgaa	gcagcaaaagagacactggcag		1231
Db	122	TGACAAAGGACATGT	TAACAAGAGTAACATGTGT	TGAAACGACGCAAGAGGCACCTGGCAG			181
Qy	1232	aaacaaacctgaa	cccttc	caaaagatggctg	aaaaagatggatgtctt	ccaatctggattca	1291
Db	182	AAAAACAACCTGA	ACCTTCCAAAGATGGCT	GA AAAAAGATGGATGCTT	CCAATCTGGATTCA		241

Qy	1292	atagagagacttcgctgggtgaataatcaactcgtgctctttttggagtttgaggatatacctag	1351
Db	242	ATGAGGAGACTTCGCTGGTGAATAATCATCACTGGCTTTTGGAGTTTGAGGTATACCTAG	301
Qy	1352	agtaacctccagaacagatitgagagttagtgaggaacaagccaagcagctgtgcagatgagta	1411
Db	302	AGTACCTCCAGAACAGATTTGAGTAGTGTGGGGAACAAGCCAGAGCTGTGCAGATGAGTA	361
Qy	1412	caaaagtccctgatccagtttcctgcagaaaaaggcaaaagaatctagatgcaataaccacc	1471
Db	362	CAAAAGTCCCTGTATCCAGTTCCTTCGACAAAAGGCAAAAGTAATCTAGATCAATAACCA	421
Qy	1472	ctgaccacaaccacaatgccagcctctgcacgaagctgcaggacacagaaccagtggtgc	1531
Db	422	CTGACCAACACCAATATGCCAGGCTGCTGACGAGAGCTGCAGGCACAGAACCACTGGTG	481
Qy	1532	aggacatgacaactcatctcattctctgcgcagcttttaaggagttctctgcagttccagcttga	1591
Db	482	AGGACATGACAACCTCATCTTCGCGAGCTTTAAGGAGTTCCTGTCAGTCCAGCTGA	541
Qy	1592	gggctctcttggcaaatgtag	1611
Db	542	GGGCTCTTCGGCAAAATGTAG	561

RESULT 12

```

US-08-469-318-57
Sequence 57, Application US/08469318
Patent No. 6022535
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,318
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,872
FILING DATE:
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 951 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-469-318-57

```

Query Match 33.1%; Score 539.2; DB 5; Length 951;
Best Local Similarity 94.4%; Pred. No. 8.9e-125;
Matches 559: Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy	1017	tcttgagggtgagggtctctgagggtgagggtctctgagcgcagtcacccccagagagaaga	1076
Db	360	TTCCCGGGTGGTGGTCTTGGCGCGCGCTCCAAACATGGCTCCAGTACCACCAAGTGAAGA	419
Qy	1077	ttccaaagatgtagcgcgcgcacacagacagacccctcttcagaacgaatgtacaa	1136
Db	420	TTCCAAAGATGTGGCGCGCCACACAGACAGCCACTCACTCTTTCAGAACGAATTGACAA	479
Qy	1137	acaaattcgtatcatcctcgacggcatctcagccctgagaagagacatgtaacaagag	1196
Db	480	ACAAATTCGGGTACATCTCGACGGGATATCAGCCCTGGAAGGGAGACATGTACAAAGAG	539
Qy	1197	taacatctgtgaagcagcaagaagagcactggcagaaacacacctgaaaccttccaaagat	1256

Db 540 TAACATGTGTGAAGCAGCAAAAGAGCGCTAGCAGAAAAACAACCTGAACCTTCCAAAGAT 599
QY 1257 gctgaaaaagatgagcttccaatcttgattcaatgagagacttgctggtgaaaat 1316
Db 600 GCGTGAAGAAAGATGGATGCTTCCAATCCGGATTCATAGGAGACATGCTGCTGGTGAAT 659
QY 1317 catcactggtctttggagtttgaggtatcacctagagtacacctccagaaacagattgagag 1376
Db 660 CATCACTGCTCTTTGGAGTTTGAGGTATACCTCGAGTACCTCCAGAACAGATTGAGAG 719
QY 1377 tagtgaggaacaagcagagctgtgcagatgagtaacaaagtctctatccagttcctgca 1436
Db 720 TAGTGAGGAACAAGCAGAGCTGTGCAGATGTGCAAAAGTCTGATCCAGTTCCTGCA 779
QY 1437 gaaaagggcaaaagatcttagatgcaataaacacccctgaccccaaccacaatgccagcct 1496
Db 780 GAAAAGGCAAAAGATCTAGATGCAATAACCAACCCCTGACCCCAACCAAAATGCATCCCT 839
QY 1497 gctgacgaagctgcaggcagacaaacagtggtgcagagacatgacaactcatctattct 1556
Db 840 GCTGACGAAGCTGCAGGCACAGACAGTGGCTGCAGGACATGACAACCTCATCTATTCT 899
QY 1557 ggcgagctttaaggagttcctgcagtcagtcagcctgagggctcttcggcaaatg 1608
Db 900 GCGCAGCTTTAAGGAGTTCTCTGCAGTCCAGCCTGAGGGCTCTTCGGCAAAATG 951

RESULT 13

PCT-US95-01185-57

; Sequence 57, Application PC/TUS9501185
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 196
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01185
; FILING DATE: 02-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192325
; FILING DATE: 14-FEB-1994
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 951 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-01185-57

Query Match 33.1%; Score 539.2; DB 6; Length 951;
Best Local Similarity 94.4%; Pred. No. 8.9e-125;
Matches 559; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1017 ttctggaggtgaggttctgaggtggaggttctgtcagccagttaccctccaggaaga 1076
Db 360 TTCCCGGGGTGGTGTCTTGGCGGGGCTTCCAACATGGCTCAGTACCACCAAGGTGAAGA 419
QY 1077 ttccaaagatgtagccgccacacagacagccactcactcttcagaaacgaattgacaa 1136
Db 420 TTCCAAAGATGTGGCGGGCCCCACACAGACAGCCACTCACCCTTTTCAGAACGAAATGACAA 479
QY 1137 acaattcgggtacatctctcagcgggcatctcagccctgagaaaggagacatgtacaagag 1196
Db 480 ACAAAATTCGGTACATCCTTCGAGCGGTATATCAGCCCTGAGAAAGGAGACATGTAAACAAG 539

QY 1197 taacatgttgaagcagcaaaagcactggcagaaaaacaacctgaacattccaagat 1256
Db 540 TAACATGTGTGAAGCAGCAAAAGAGCGCTAGCAGAAAAACAACCTGAACCTTCCAAAGAT 599
QY 1257 gctgaaaaagatgagcttccaatcttgattcaatgagagacttgctggtgaaaat 1316
Db 600 GCGTGAAGAAAGATGGATGCTTCCAATCCGGATTCATAGGAGACATGCTGCTGGTGAAT 659
QY 1317 catcactggtctttggagtttgaggtatcacctagagtacacctccagaaacagattgagag 1376
Db 660 CATCACTGCTCTTTGGAGTTTGAGGTATACCTCGAGTACCTCCAGAACAGATTGAGAG 719
QY 1377 tagtgaggaacaagcagagctgtgcagatgagtaacaaagtctctatccagttcctgca 1436
Db 720 TAGTGAGGAACAAGCAGAGCTGTGCAGATGTGCAAAAGTCTGATCCAGTTCCTGCA 779
QY 1437 gaaaagggcaaaagatcttagatgcaataaacacccctgaccccaaccacaatgccagcct 1496
Db 780 GAAAAGGCAAAAGATCTAGATGCAATAACCAACCCCTGACCCCAACCAAAATGCATCCCT 839
QY 1497 gctgacgaagctgcaggcagacaaacagtggtgcagagacatgacaactcatctattct 1556
Db 840 GCTGACGAAGCTGCAGGCACAGACAGTGGCTGCAGGACATGACAACCTCATCTATTCT 899
QY 1557 ggcgagctttaaggagttcctgcagtcagtcagcctgagggctcttcggcaaatg 1608
Db 900 GCGCAGCTTTAAGGAGTTCTCTGCAGTCCAGCCTGAGGGCTCTTCGGCAAAATG 951

RESULT 14

PCT-US94-12873-3

; Sequence 3, Application PC/TUS9412873
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: HYBRID CYTOKINES
; NUMBER OF SEQUENCES: 26
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44Mb, double side, high density
; OPERATING SYSTEM: MS-DOS Version 6
; SOFTWARE: WORD for WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12873
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
PCT-US94-12873-3

Query Match 33.1%; Score 538.4; DB 6; Length 540;
Best Local Similarity 99.8%; Pred. No. 1.2e-124;
Matches 539; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1072 gaagattccaaagatgtagcccccacacagacagccactcacctcttcagaaacgaatt 1131
Db 1 GAAGATTCCAAAGATGTAGCCGCCCCACACAGACGCCACTCACCTCTTCAGAACGAAT 60
QY 1132 gacaaacaaattcgggtacatctctgacggcctatctcagccctgagaaaggagacatgtaac 1191
Db 61 GACAAACAAATTCGGTACATCTCGAGCGCATCTCAGCCCTGAGAAAGGAGACATGTAA 120
QY 1192 aagagtacaatgtgaaagcagcaaaaggcactggcagaaaaaacacctgaacctcca 1251
Db 121 AAGAGTAAATGTGTGAAAGACGACAAAGAGGACTGGCAGAAAAACCAACCTGAACCTTCCA 180
QY 1252 aagatggctgaaaaagatggatgcttccaatctggattcaatgaggagacttgctgggtg 1311

[illegible]

RESULT 15

US-08-567-047-1
: Sequence 1, Application US/08567047
: Patent No. 5789552
: Patent No. 5789552 5789555
: GENERAL INFORMATION:
: APPLICANT: SAVINO, Rocco
: APPLICANT: LAHM, Atmin
: APPLICANT: CILIBERTO, Gennaro
: TITLE OF INVENTION: METHOD FOR SELECTING SUPERAGONISTS,
: TITLE OF INVENTION: ANTAGONISTS AND SUPERANTAGONISTS FOR HORMONES HAVING
: TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/567,047
: FILING DATE: 04-DEC-1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/387,924
: FILING DATE: 23-FEB-1995
: APPLICATION NUMBER: IT RM93A000409
: FILING DATE: 23-JUN-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, Roger L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/DOCKET NUMBER: SAVINO=1
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: TELEX: 248633
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 555 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA

Result No.	Query	Score	Match	Length	DB	ID	Description
1	1627	100.0	1627	1	T97848	Human fusion polyp	
2	1457	89.6	1552	1	T97849	Human fusion polyp	
3	995	61.2	2061	1	N90340	Sequence encoding	
4	995	61.2	2066	1	Q41746	IL-6 receptor codi	
5	995	61.2	2087	1	N09847	DNA contg. region	
6	995	61.2	3319	1	V60295	Human interleukin-	
7	993.4	61.1	1486	1	V60296	Human interleukin-	
8	993.4	61.1	3319	1	T31441	Interleukin-6 rece	
9	969	59.6	1074	1	V04440	Interleukin 6 rece	
10	565.2	34.7	1139	1	N90255	Interleukin-6. New	
11	565.2	34.7	1139	1	N80299	Interleukin 6. Pro	
12	565.2	34.7	1162	1	Q01763	BSF-2 gene for hum	
13	563.6	34.6	1101	1	N90131	DNA sequence of pB	
14	563.6	34.6	1101	1	N90135	DNA sequence of pB	
15	563.6	34.6	1101	1	N90345	Plasmid pBSF2-L8	
16	563.6	34.6	1128	1	Q74057	Human interleukin-	
17	563.6	34.6	1128	1	V60294	Human interleukin-	
18	563.6	34.6	1145	1	N90377	Interferon-beta-2	
19	563.6	34.6	1145	1	N70348	Sequence of human	
20	563.6	34.6	1145	1	Q39582	IFN-beta-2a coding	
21	563.6	34.6	1145	1	Q86523	cDNA encoding inte	
22	563.6	34.6	1161	1	N81460	Sequence encoding	
23	562	34.5	1101	1	N80966	Plasmid pBSF2-L8.	
24	562	34.5	1101	1	N81517	Sequence encoding	
25	558.8	34.3	1099	1	Q25831	Mutant human BCDP.	
26	558	34.3	1165	1	Q56265	Sequence of human	
27	555	34.1	639	1	N91706	Human interleukin-	
28	554	34.1	1162	1	Q11824	B cell differentia	
29	552.2	33.9	566	1	N80300	Interleukin 6. Pro	
30	551.8	33.9	555	1	Q85465	Mutant Interleukin	
31	550.4	33.8	561	1	Q36903	Human Interleukin	
32	550.4	33.8	561	1	Q30773	Human Interleukin	
33	549	33.7	560	1	Q03365	Segment of human B	

PS Disclosure; Fig 3; 63pp; English.
CC The cDNA in N90340 was derived from monocyte cell line U937.
CC Isolated BSE2 receptor and DNA encoding it are claimed, as are
CC (b) expression vectors; (c) host organisms; (d) antibodies; and
CC (e) hybridomas.
SQ Sequence 2061 BP; 418 A; 631 C; 621 G; 391 T;

```
Query Match      61.2%; Score 995; DB 1; Length 2061;
Best Local Similarity 100.0%; Pred. No. 6.8e-242;
Matches 995; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 catgagtggttagccgaggaagacatgctgcccgcgtgcgcgtgcgtgctgctccc 67
    |||
Db 221 CATGAGTGGTAGCGAGGAGAGCATGCTGGCGCTGCGCTGCGCTGCTGCTGCTGCC 280

Qy 68 tgcctgcccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 127
    |||
Db 281 TCCTGGCCGCGCGGAGCGCGCTGGCGCCCAAGGCGCTGCCCTGCGCAGGAGTGCAA 340

Qy 128 gaggcgtgctaccagtgctgcagagagacagctgactctgacccgcccgggtagagc 187
    |||
Db 341 GAGGCGTCTGACCATGCTGCGAGGAGACAGCGTACTCTGACCTGCGCGGGGTAGAGC 400

Qy 188 cgaagacaatgcactgttactggtgctcaggaagccgctgcaggtcccccacccca 247
    |||
Db 401 CGGAAGACAATGCCACTGTTACTGGGTCTCAGGAAGCCGCTGCAGGCTTCCACCCCA 460

Qy 248 gagatgggtgctgaggaagagctgctgctgaggtcggtgcagctccacactctg 307
    |||
Db 461 GCAGATGGCTGGCATGGGAAGAGGCTGCTGCTGAGTCTGCTGAGTCCAGCTCCAGCTCTG 520

Qy 308 gaaactattcatgctaccagtcgcagagagacagctgactctgactgctgctgagtg 367
    |||
Db 521 GAAACTATTTCATGCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 580

Qy 368 tccccccgagagccagctctctctctctctctctctctctctctctctctctctct 427
    |||
Db 581 TTCCCCCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 640

Qy 428 gtgagtggtgctcctgagagaccccatcctctgacacaaagagctgtctgttgagga 487
    |||
Db 641 GTGAGTGGGTCTCGGAGACCCCATCCCTGACGACAAAGGCTGTGCTTGTGTGAGGA 700

Qy 488 agttcaaacagtcgcccagagacttccagagccgtgcccagtatcccccagagctccc 547
    |||
Db 701 AGTTTTCAGAACAGTCCGGCCGAGACTTCCAGAGCCGCTGCCAGTATTCCACGAGTCC 760

Qy 548 agaagtctctcctgccagtttagcagtcctccgagggagagacagctcttctacatagtcca 607
    |||
Db 761 AGAAGTTCTCCTGCCAGTTAGCAGTCCCGGAGGAGACAGCTCTTCTTACATAGTGCCA 820

Qy 608 tbtgctcgcagtagtgctgggagcaagttagcaaaaactcaaaccttcaaggttag 667
    |||
Db 821 TGTGCTGCCAGTAGTGTGCGGAGCAAGTTTCAGAAAACACTCAAACTTTCAGGGTTGTG 880

Qy 668 gaactctgagctgactgcgcctgcaacatcacagtcactcctggtgcccagaaaaccccc 727
    |||
Db 881 GAATCTTGACGCTGATCGCTGCCACATCACAGTCACTGCGCTGCCAGAAACCCCC 940

Qy 728 gctggctcagtgctacctggcagacccccactcctctggaactcaattcttctacagactac 787
    |||
Db 941 GCTGGCTCAGTGTACCTGGCAAGACCCCACTCTCTGGAACATCATCTTTCTACAGACTAC 1000

Qy 788 ggtttgagctcagatagctgggtgaacgtcaagacattcaacatgagtggtcaag 847
    |||
Db 1001 GGTTTGAGCTCAGATATCGGGTGAACGGTCAAGACATTCAACATGGATGGTCAAGG 1060

Qy 848 acctcagcactgctgctcaccagcgcctggagggcctgagcgacgtggtgacgc 907
    |||
Db 1061 ACTTCAGCATCATCTGTGTATCCACGACGCTGGAGCGCGCTGAGGCACGTTGGTCAAC 1120

Qy 908 ttcgtgcccagggaggttctcggaagggcagtgagtgagtgagtgagtgagtgagtgag 967
    |||
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Db 1121 TTCTCTGCCAGGAGGAGTTTCGGCAAGGCGAGTGGAGCGAGTGGAGCCGGAGCCATGG 1180
    |||
Qy 968 gacgccttgacagaatccagagctccagct 1002
    |||
Db 1181 GCACGCTTGGACAGAATCCAGGAGTCTCTCCAGCT 1215

RESULT 4
Q41746
ID Q41746 standard; DNA; 2066 BP.
AC Q41746;
DT 13-SEP-1993 (first entry)
DE IL-6 receptor coding sequence.
KW Interleukin-6; IL-6; receptor; immunoglobulin-like; domain; truncated;
KW transmembrane; multiple myeloma; binding; ability; signal transfer;
KW disease; intracellular; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT cds 226..1632
    /*tag= a
FT J05001892-A.
PN 16-APR-1993.
PF 02-OCT-1991; 255521.
PR 02-OCT-1991; JP-255521.
PA (CHUS ) CHUGAI PHARM CO LTD.
PA (KISH/) KISHIMOTO C.
PA (TOYJ ) TOSOH CORP.
DR WPI; 93-161739/20.
DR P-PSDB; R37215.
DT New interleukin-6 receptor deriv. - for treating diseases caused
PT by IL-6, e.g. multiple myeloma
PS Disclosure; Page 10-12; 23pp; Japanese.
CC This sequence encodes an interleukin-6 (IL-6) receptor. Variants of
CC the receptor lacking either the immunoglobulin-like domain or the
CC transmembrane and intracellular domain have IL-6 binding ability and
CC signal transfer ability. Either the full length or truncated IL-6
CC receptors may be used for diseases caused by IL-6 such as multiple
CC myeloma.
SQ Sequence 2066 BP; 420 A; 642 C; 615 G; 389 T;
```

```
Query Match      61.2%; Score 995; DB 1; Length 2066;
Best Local Similarity 100.0%; Pred. No. 6.8e-242;
Matches 995; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 catgagtggttagccgaggaagacatgctgcccgcgtgcgcgtgcgtgctgctccc 67
    |||
Db 200 CATGAGTGGTAGCGAGGAGAGCATGCTGGCGCTGCGCTGCGCTGCTGCTGCC 259

Qy 68 tgcctgcccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 127
    |||
Db 260 TCCTGGCCGCGCGGAGCGCGCTGGCGCCCAAGGCGCTGCCCTGCGCAGGAGTGCAA 319

Qy 128 gaggcgtgctaccagtgctgcagagacagctgactctgactgcccgggtagagc 187
    |||
Db 320 GAGGCGTCTGACCATGCTGCGCAGGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 379

Qy 188 cgaagacaatgcactgttactggtgctcaggaagccgctgacaggtcccccacccca 247
    |||
Db 380 CGGAAGACAATGCCACTGTTACTGGTGTCTCAGGAAGCCGCTGCAGGCTTCCACCCCA 439

Qy 248 gcatgagtggtggaatggaagaggtgctgctgaggtcggtgagctccacactctg 307
    |||
Db 440 GCAGATGGCTGGCATGGGAAGAGGCTGCTGCTGAGTCTGCTGAGTCTCAGCTCTG 499

Qy 308 gaaactattcatgctaccagtcgcagagagacagctgactgctgctggtgagtg 367
    |||
Db 500 GAAACTATTTCATGCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 559

Qy 368 tccccccgagagccagctctctctctctctctctctctctctctctctctctctct 427
    |||
Db 560 TTCCCCCGGAGGAGCCCAAGCTCTCTGCTTCCCGAAGAGCCCGCTCAGCAATGTGTTT 619
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Qy	428	gtgaagtgagggtcctcggagacaccccatcctgacacaaaggctgtgctcttggtgagga	487
Db	620	GTGAGTGGGGTCTCGGAGCACCCCATCCTTCACGACAAAGGCTGTGCTTGGTGAGGA	679
Qy	488	agttcagaacagtccgcccgaagacctccagagaccctgccagtattccagagatccc	547
Db	580	AGTTTCAGAACAGTCCGGCCGAAGACTTCCAGAGCCGTGCCAGTATTTCCACGAGATCCC	739
Qy	548	agaagtctcctccagtttagcagtcgccgagggagagacagctctttctacatagtgtcca	607
Db	740	AGAAATTTCTCTGCCAGTTAGCAGTCCCGAGGGAGACAGACTTTCTACATAGTGTCCA	799
Qy	608	tgtgctgcgcagtagtgcgggagcaagtttcagcaaacctcaaacctttcagggtgtg	667
Db	800	TGTGCGTCCGACGTAAGTTCGGGAGCAAGTTTCAGCAAAACTCAAACCTTTCAGGTTGTG	859
Qy	668	gaatcttgagcctgacgcctgcacacatcacagtcacgtcacgtccgtggcagaagaaccccc	727
Db	860	GAATTTTGCAGCTGATTCGCGCTTGCACATCACAGTCACCTGCCGTGGCCAGAAACCCCC	919
Qy	728	gctggtccagtgtcacctgtgcaagaccccccaactcctggaactcatctttcacagctac	787
Db	920	GCTGGCTCACTGTACCTGGCAAGACCCCACTCTCGAATCATCTTTCTACAGACTAC	979
Qy	788	ggttgagctcagatcgggtgtaacggtcgaagacattcacacaatcggatgtcaagg	847
Db	980	GGTTTGAGCTCAGATATCGGGCTGAACGGTCAAGACATTCACAACATGGATGGTCAAGG	1039
Qy	848	acctcagaatactgtgtcatccagcaagcctgagcgccctgaagcaactggtgacgc	907
Db	1040	ACCTCCAGCATCACTGTGTATCCAGACGCCCTGAGCGGCTGAGGACCGCTGTGTGCAGC	1099
Qy	908	ttcgtgccagggaggttcgaggcaagcgagtgagcgagtgagcgagcccgagccatgg	967
Db	1100	TTCGTGCCCAAGGAGGATTCGGGCAGGCGCACTGGAGCGCATGGAGCGCCCGGAGGCCATGG	1159
Qy	968	gcagccttgacagaatccaggagtcctccagct 1002	
Db	1160	GCAGCGCTTGACAGAGAATCCAGGAGTCTCCAGCT 1194	
RESULT	5		
N90847			
ID	N90847	standard; DNA; 2087 BP.	
AC	N90847;		
DT	23-JAN-1990	(first entry)	
DE	DNA contg. region encoding BSF2 receptor.		
KW	B cell stimulating factor-2 receptor; monocytic U937 cell line.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	cds	247..1650	
FT		/*tag= a	
FT	misc_feature	250..312	
FT		/*tag= b	
FT	misc_feature	1330..1404	
FT		/*tag= c	
PN	AU8928720-A.		
PD	27-JUL-1989.		
PF	23-JAN-1989; 28720.		
PR	22-JAN-1988; JP-012387.		
PR	25-JAN-1988; JP-012599.		
PR	04-AUG-1988; JP-194885.		
PR	14-JAN-1989; JP-007461.		
PA	(KISH) Tadami Kishimoto.		
PI	Kishimoto T.		
DR	WR; 89-264012/37. P-PSDB; P90525.		
RT	Receptor protein for human B cell stimulating factor-2 - used for		
PT	developing prophylactic, therapeutic and diagnostic agents for		
PT	associated disorders.		
FS	Disclosure; fig 3.1-3.5; 76pp; English.		
CC	The DNA contains a region encoding the BSF2 receptor derived from a		
CC	monocytic U937 cell line. It is used to produce large amts. of receptor		

[illegible]

Thu Aug 10 17:14:03 2000

Qy 968 gcaagccttgacagaatccaggagtccctccagct 1002
 |||||
Dh 1181 GCAGCCTTGGACAGAATCCAGGAGTCCTCCAGCT 1215

RESULT 6

VI	V60295 standard; DNA; 3319 BP.	
ID	V60295;	
AC	V60295;	
DT	02-FEB-1999 (first entry)	
DE	Human interleukin-6 receptor cDNA.	
KW	Interleukin-6 receptor; human; hepatitis B virus; HBV; infection;	
KW	therapy; ss.	
OS	Homo sapiens.	
PN	W09835694-A2.	
PD	20-AUG-1998.	
PF	10-FEB-1998; U08898.	
PR	11-FEB-1997; US-795473.	
PA	(DAVID/) DAVISIT MEDICAL RES SERVICES & DEV.	
PA	(HADA-) HADASIT MEDICAL RES SERVICES & DEV.	
WP	WI: 98-520755/44.	
DR	Treatment of hepatitis B virus infection - using a soluble active	
PT	agent which prevents interaction of HBV with hepatocytes mediated by	
PT	human interleukin 6	
PS	Disclosure; Fig 6a-b; 51pp; English.	
CC	This is a previously reported nucleotide sequence for human	
CC	interleukin-6 (hil-6) receptor mRNA. The invention relates to the	
CC	finding that hil-6 is essential for hepatitis B virus (HBV)	
CC	infection. The invention provides a pharmaceutical composition for	
CC	the treatment of HBV infection, comprising a soluble active agent	
CC	that interacts with at least one of the binding sites between hil-6	
CC	and the p51 region of HBV and between hil-6 and hepatocytes and	
CC	other HBV-permissive cells. The active agent competitively binds	
CC	to at least one of these sites and thereby prevents hil-6-mediated	
CC	HBV infection of hepatocytes and other HBV-permissive cells. The	
CC	soluble active agent is selected from glycoprotein 80 (gp80) having	
CC	receptor sites which interact with hil-6, soluble glycoprotein 130	
CC	(gp130) having receptor sites which interact with hil-6, hil-6	
CC	derived peptide Lys41-Ala56, hil-6 derived peptide Gly77-Glu95,	
CC	hil-6 derived peptide Gln153-His165, a combined 1 and 2 hil-6	
CC	mutant (mhil-6 1+2), and mhil-6 1+2 substituted with Phe171 to Leu	
CC	and Ser177 to Arg, and mixtures of any of these.	
CC	Sequence 3319 BP; 735 A; 936 C; 961 T;	
NO		

Query Match 61.2%; Score 995; DB 1; Length 3319;
Best Local Similarity 100.0%; Pred. No. 8.2e-242;
Matches 995; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	8	catgagtggttagcccgaggaagaacatgctgccctcagctcgctcgcttggtcgcc	67
Db	412	CATGAGATGGTAGCCGAGGAAGCATGTGCCGCTGCGCTGCCGCCTGCTGGCTGCC	471
QY	68	tgctggccgcgcgcggagcgcgtggccccaaaggcgtgccctgcgcgaggaggtggcaa	127
Db	472	TGCTGGCCGCGCGGAGCGCGCTGGCCCCAAGGCGCTGCCCTGGCGCAGAGGTGGCAA	531
QY	128	gaggcgctgtgaccaagtctgcagagagacagctgactctgactcaccgcgggggtagac	187
Db	532	GAGGCGTGCTGACCATGTGCCCAGGAGACAGCGTGACTCTGACCTGCCCGGGGTTAGAC	591
QY	188	cgaagaacaaatgccactgttcactgggtgctcagaagaacgcggtgcagggtcccacccc	247
Db	592	CGGAAGACAATGCCACTGTTCACTTGGTGCTCAGGAAGCGGGTGCAAGGTCCTCCACCCCA	651
QY	248	gcagatgggctggcatgggaaggagctgtctgtcgaagtgcgttcagctccacgactctg	307
Db	652	GCAGATGGGCTGGCATGGGAAGGAGGTGCTGCTGAGGTCGGTGACCTCCAGACTCTG	711
QY	308	gaaaactattcatgctaccgggcgcgcgcccaagctgggaactgtgcacttgcgtggtagtg	367
Db	712	GAACTATTCTAGCTACCGGCGCGCGCCCGCCAGCTGGACTGTGCATCTGCTGGTGGATG	771

Qy	368	tccccccgagagcccaagctctcctgcttcgaaagagccctcagcaattgtttt	427
Db	772	TTCCCCCGAGGAGCCCCAGCTCTCTGTTCCGGAACAGCCCCCTCAGCAATGTTGTTT	831
Qy	428	gtgagtgggtctctcgagacaccccatcctgaacacaaaagctgtgctcttggtagga	487
Db	832	GTGAGTGGGTCTCTCGAGCACCCATCCTGACGACAAAGAGCTGTGCTCTGTGTGAGGA	891
Qy	488	agtttcagaacactccgccgaagactccagagagccgtgccagtattccccaggaagtccc	547
Db	892	AGTTTTCAGAACAGTCCGGCGGAGAGACTTCCAGAGCCGTCGCAGTAATTCCCCAGGAGTCCC	951
Qy	548	agaagtctcctgccagtttagcagtcctccggaggaggagcaagctctttttacatagtgcca	607
Db	952	AGAAATTTCTCTGCCAGTTAGCAGTCCCGGAGGGGAGACAGCTCTTTCTACATAGTGTCCA	1011
Qy	608	tgtcgtcgcgcagtagtgttcgggagcaagttcagcaaaactcaaacctttcagggtgtg	667
Db	1012	TGTGCGTGGCCAGTAGTGTGCGGAGCAAGTTCAGCAAAACTCAAACCTTTCAGGGTTGTG	1071
Qy	668	gaattctgcagctgtatccgcctgcccacatcacagtcactgcctggccagaagaccccc	727
Db	1072	GAATCTTGCAGCCTGTATTCGCCCTGCCAAACATCACAGTCACTGCCGTGGCGAAGAACCCCC	1131
Qy	728	gctggctcagtgctcaactggcaagacccccactcctggaaactcatctttcacagactac	787
Db	1132	GCTGGCTCAGTGTACCTGCGAAGACCCACATCCTTGGAAACTCATCTTTCTACAGACTAC	1191
Qy	788	ggtttgagctcaagatctggggctgaacggtcaaaagcattcaacatggatgggtcgaag	847
Db	1192	GGTTTGAAGCTCAGATATCGGGCTGAACGGTCAAAAGACATTCACACATGGATGGTCAAGG	1251
Qy	848	accttcagcatcactgtgtcatccacgacgcttggagcgccctgaggcacgtgggtgcagc	907
Db	1252	ACCTCCAGCATCTGTGTCATCCACGACGCCCTGGAGCGCCTGAGGCACTGTGTGCAGC	1311
Qy	908	ttcgtgccagagaggttcgggcaagcgagtggaacagagtgagcccgaggggccatgg	967
Db	1312	TTCTGTGCCAGGAGGAGTTGCGGCGAAGCGGAGTGGAGCGAGTGGACCCCGAGGCCATGG	1371
Qy	968	gcacgccttggacagaatccaggaggtcctccagct	1002
Db	1372	GTACGCTTTGGACAGAAATCCAGGAGTCTCCAGCT	1406

RESULT

V60296	ID	V60296 standard; DNA; 1486 BP.
AC	V60296;	
AC	02-FEB-1999	(first entry)
DE	Human interleukin-6 nucleotide sequence.	
DE	Human interleukin-6 nucleotide sequence.	
KW	Interleukin-6; human; hepatitis B virus; HBV; infection; therapy;	
KW	ss.	
OS	Homo sapiens.	
PN	WO9835694-A2.	
PN	20-AUG-1998.	
PD	10-FEB-1998;	U08898.
PF	10-FEB-1998;	U08898.
PF	11-FEB-1997;	US-795473.
PR	(DAVI/) DAVIDSON C M.	
PA	(HADA-) HADASIT MEDICAL RES SERVICES & DEV.	
PA	WPI; 98-520755/44.	
DR	Treatment of hepatitis B virus infection - using a soluble active	
PT	agent which prevents interaction of HBV with hepatocytes mediated by	
PT	human interleukin 6	
PT	human interleukin 6	
PT	disclosure; Fig 7; 51pp; English.	
FS	This is a previously reported nucleotide sequence for human	
CC	interleukin-6 (hIL-6). The invention relates to the finding that	
CC	hIL-6 is essential for hepatitis B virus (HBV) infection. The	
CC	invention provides a pharmaceutical composition for the treatment	
CC	of HBV infection, comprising a soluble active agent that interacts	
CC	with at least one of the binding sites between hIL-6 and the pS1	
CC	region of HBV and between hIL-6 and hepatocytes and other	
CC	HBV-permissive cells. The active agent competitively binds to at	

CC	least one of these sites and thereby prevents hIL-6-mediated HBV infection of hepatocytes and other HBV-permissive cells. The soluble active agent is selected from glycoprotein 80 (gp80) having receptor sites which interact with hIL-6, soluble glycoprotein 130 (gp130) having receptor sites which interact with hIL-6, hIL-6 derived peptide Lys41-Ala56, hIL-6 derived peptide Gly77-Glu95, hIL-6 derived peptide Gln153-His165, a combined 1 and 2 hIL-6 mutant (mhIL-6 1+2), and mhIL-6 1+2 substituted with Phe171 to Leu CC and Ser177 to Arg, and mixtures of any of these.	Query Match Best Local Similarity 99.9%; Pred. No. 1.5e-241; Matches 994; Conservative 0; Mismatches 1; Indels 0; Gaps	61.1%; Score 993.4; DB 1; Length 1486; 99.9%; Pred. No. 1.5e-241; Matches 994; Conservative 0; Mismatches 1; Indels 0; Gaps
Qy	8 catggagtgttagccgaggaggagcatgctggcgtcgagctgcgcgtgcgtgctgctgccc 67		
Db	26 CATGGAGTGTAGCCGAGGAGGAGCATGTGGCCGTGCGCTGCGCGCTGCTGGCGTCCC 85		
Qy	68 tgcctggccgcgcgggagcgcgctggccccaaaggcgctgcccgcgcgcgcgcgcgcgc 127		
Db	86 TGCTGGCCGCCCGGGAGCGCGCTGSCCCCAAGGCGCTGCCCTGCGCAGGAGGTGCGCA 145		
Qy	128 gaggcgtgctgaccagctctccaggagagacgctgactctgacctgcccgcggggtagagc 187		
Db	146 GAGCGTGTCTGACCACTCTCCAGGAGACACGCTGACTCTGACCTGCCCGGGGTAGAC 205		
Qy	188 cgaagacaatgccactgttcactgggtgctcaggaagcggcgtcagagctccaccacca 247		
Db	206 CGGAAGACAATGCCACTGTTACTTGGTGTCTCAGGAAGCGGCTGCAGGCCTCCACCCCA 265		
Qy	248 gcagatgggctggcatgggagagcgctgctgtagtgctggcgagctccacgactctg 307		
Db	266 GCAGATGGCTGGCATGGGAGGAGGCTGCTGCTGAGGTGGTGCAGCTCCACGACTCTG 325		
Qy	308 gaaactattcatgtaccggcgccggccgcagctgggactgtgcactgtcgtgtggtgatg 367		
Db	326 GAAACTATTCTATGCTACCGGGCGGGCGCCAGCTGGGACTGTGCCTGCTGCTGGATG 385		
Qy	368 ttccccccgaggagcccaagctcctgcttcggaagagccccctcagcaaatgtgttt 427		
Db	386 TTCCCCCCGAGGAGCCCACTCTCTCTGCTTCGGAAGAGCCCCCTCAGCAATGTTGTTT 445		
Qy	428 gtgagtgggtccttcggagcaccccatccctgacgacaaaggctgtgctctctgttgagga 487		
Db	446 GTGAGTGGGTCTCTCGGAGCACCCCATCCCTGACGACAAAGGCTGTGCTCTGGTCAGGA 505		
Qy	488 agtttcagaacagtcocggccgaagacttccaggagccgtgccaagtattcccaggagctcc 547		
Db	506 AGTTTTCAGAACAGTCCCGCCGGAAGACTTCCAGGAGCGCTGCCAGTATTCCACGAGTCCC 565		
Qy	548 aagaattctcctgcaattagcagctccggaggagagacagctctttctacatagtgtcca 607		
Db	566 AGAAGTTCTCTCGCACTTACAGTCCCGGAGGAGACAGCTCTTCTTCATATAGTCTCCA 625		
Qy	608 tgtcgtcgccagtagtgtcgggagcaagttccagcaaaactcaaacctttcagggtgttg 667		
Db	626 TGTGCGTCCGCACTAGTGTGCGGAGCAAGTTTCAGCAAACTCAAACTTTCAGGTTGTG 685		
Qy	668 gaattctgacgctgatccgcctgccaacatcacagtccactgcgtgcccagaaaccccc 727		
Db	686 GAATCTTGACGCTGATCCGCCCTGCCAACATCATCAGTCACTGCGGTGGCCAGAAACCCCC 745		
Qy	728 gctggtcagtgctaacctggcagaagaccccccaactccttggaactcatottttcacagctac 787		
Db	746 GCTGGCTTCAGTGTACCTGCAAGACCCCACTCCCTTGGAACCTCATCTTTCTACAGACTAC 805		
Qy	788 gggttgagctcagatctcgggctgaacggtgcaagcattcacaacatggatggtcaagg 847		
Db	806 GGTTTGAGCTCAGATATCGGGCTGAACGGTCAAGAGCATTTCAACAACATGGATGGTCAAG 865		
Qy	848 acotccagcatcactgtgtcatccacgacgcctggagcgctcgagcgacgttggtgcagc 907		

Db	866	ACCTCCAGCATCACTGTGTCTATCCAGACGCCTGGAGCGCCTGAGCAGCTGGTCAGC	925		
Qy	908	ttctgtccaggagaggttcggcgaagcgagtgagcagtagtagaccgcgagagccatg	967		
Db	926	TTCGTGCCAGCAGAGATTTGGGCAAGCGAGTGGAGCGAGTGGAGCCGAGGCCATGG	985		
Qy	968	gcacgccttgacagaatccaggagtgctccagct	1002		
Db	986	GCACGCCTTGACAGAAATCCAGGAGTCTCCAGCT	1020		
RESULT 8					
ID	T31441	T31441 standard; cDNA; 3319 BP.			
AC	T31441;				
DC	28-NOV-1996	(first entry)			
DE	Interleukin-6 receptor coding sequence.				
KW	Interleukin-6; IL; receptor; antisense oligonucleotide; inhibition;				
KW	gene expression; kidney tumour; myeloma; Kaposi's sarcoma; psoriasis;				
KW	rheumatoid arthritis; endotoxic shock; ss.				
OS	Homo sapiens.				
FH	Key	Location/Qualifiers			
FT	cds	438..1844			
FT		/*tag= a			
FT		/product= Interleukin-6 receptor.			
FN	WO9618416-A1.				
PD	20-JUN-1996.				
PF	15-DEC-1995; J02587.				
PR	16-DEC-1994; JP-313167.				
PR	18-AUG-1995; JP-210739.				
PA	(CHUS) CHUGAI SEIYAKU KK.				
PI	Koishibara Y, Kuromaru K;				
DR	WPI: 96-300392/30.				
DR	P-PSDB; R98364.				
PT	Anti-sense oligo:nucleotide inhibitor against human IL-6R expression				
PT	- for treatment of e.g. tumours, cancers, rheumatoid arthritis,				
PT	psoriasis, endo:toxic shock, etc.				
PS	Claim 2: Page 17-21; 32pp; Japanese.				
CC	Antisense oligonucleotides may be used to inhibit the expression of				
CC	the interleukin-6 receptor. Inhibition of expression of the				
CC	IL-6 receptor is useful in the treatment of kidney tumours, myeloma,				
CC	Kaposi's sarcoma, rheumatoid arthritis, psoriasis and endotoxic				
CC	shock. The antisense oligonucleotides are administered at a dosage				
CC	of 0.1-100mg/kg, pref. 0.1-50 mg/kg,				
CC	Sequence 3319 BP; 735 A; 937 C; 960 G; 687 T;				
Query Match 61.1%; Score 993.4; DB 1; Length 3319;					
Best Local Similarity 99.9%; Pred. No. 2.1e-241;					
Matches 994; Conservative 0; Mismatches 1; Indels 0; Gaps					
Qy	8	catgagatgtagccgaggaggaaagatgtgcccgtcgactgcgagctgctggtcgtgcgc	471		
Db	412	CATGAGTGTGTAGCCGAGGAGGAGCATGTGCGCGCTCGGCTCGGCTGCTGGCTGCC	471		
Qy	68	tgctggccgcccgggagcgcgctggtcccaaggcgactacctcgcgagaggtgagca	127		
Db	472	TGCTGGCCGCCCGGAGCGGCGCTGCCCCAAGCGCTGCCCTGGCAGAGAGTGGCAA	131		
Qy	128	gagcgctgctgaccagtcctgcaggagacagcgtagactcgacctgcccgggggtagagc	187		
Db	532	GAGCGCTGCTGACCAGTCTGCCAGGACACGCTGACTCTGACCTGCCCGGGGTAGAGC	591		
Qy	188	cggaaagacaatgccaactgttcaactgggtgctcaggaaagccgggtgaggtctccaccca	247		
Db	592	CGGAAGACAATGSCACACTGTTCACTTGGCTGCTCAGGAAGCCGGTGGAGGCTCCACCCCA	651		
Qy	248	gcacatggctggcatgggaagagcgtgctgctgaggtcggtgcagctccacgactcg	307		
Db	652	GCACATGGGCTGGCATGGGAAGGAGGCTGCTGCTGAGGTCGGTGGTGCAGACTCTG	711		
Qy	308	gaacattatcatgctacccggcgccgcagctggagactgtagcttactgtggtgtagt	367		

Db 781 CGGTCAAGACATTCACAAATGGATGGTCAAGGACCTCCAGGACATCACTGTGTCAATCCAC 840
 QY 874 gacgcctggagcgccctgagcgacgtggtgcagctttctgtcccgagggaggttcgggcaa 933
 Db 841 GACGCTGGAGCGCCTGAGCAGCTGGTGCAGCTTGTGTCGCCAGGAGGAGTTTCGGCAA 900
 QY 934 ggcagtgagcgagtgagcgcccgaggcgccatggcgacgccttggacagagaatccagaggt 993
 Db 901 GCGGAGTGGAGCGAGTGGAGCGCGGAGGCCATGGCAGCGCTTGGACAGAATCCAGGAGT 960
 QY 994 cctccagct 1002
 Db 961 CTCCAGCT 969
 RESULT 10
 N90255
 ID N90255 standard; DNA; 1139 BP.
 AC N90255;
 DT 1-NOV-1989 (first entry)
 DE Interleukin-6.
 KW Interleukin-6; lysine-depleted variant; site-directed
 KW mutagenesis; human.
 OS Homo sapiens
 FH Key Location/Qualifiers
 FT cds 51..686
 FT /*tag= a
 PN WO8905824-A.
 PD 29-JUN-1989.
 PF 22-DEC-1986; U04633.
 PR 23-DEC-1987; US-137043.
 PA (GENE-) Genetics Inst Inc.
 PI Shaw G;
 DR WPI: 89-206594/28.
 DR P-PSDB; P90469.
 PT New lysine depleted variants of polypeptide
 PT - opt. modified with hydrophilic residues,
 PT biologically active but with altered solubility, stability etc.
 PS Disclosure; fig 3; 35pp; English.
 CC DNA of interleukin-6 (see corresp. P90469). Used in the patent
 CC to create lysine depleted variants by site-directed mutagenesis, or
 CC synthesis.
 CC Sequence 1139 BP; 361 A; 240 C; 231 G; 307 T;
 SQ
 Query Match 34.7%; Score 565.2; DB 1; Length 1139;
 Best Local Similarity 99.5%; Pred. No. 1.6e-133;
 Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1057 ccagtagcaccgagagaagattccaaagatgtagccgccccacacagacagccactcacc 1116
 Db 135 CCAGTACCCCGAGAGAAGATTCCAAAGATGTAGCGCGCCCCACACAGACAGCCACTCACC 194
 QY 1117 tcttcagaagaattgacaaacaaattcgggtacatctctcgacggcatctcagccctgaga 1176
 Db 195 TCYTTCAGAACGAATTGACAAACAATTCGGTACATCTCTCAGCGCATCTCAGCCCTGAGA 254
 QY 1177 aaggagacatgtaacagagtaacatgtgtgaaagcagcaaaaggcactggcagaaaaac 1236
 Db 255 AAGGAGACATGTAAACAGAGTAACATGTGTGAAAGCAGCAAAAGGCGACTTGGCAGAAAAAC 314
 QY 1237 aacctgaacctccaagatggctgaaaaagatggatgcttccaattctgattcaatgag 1296
 Db 315 AACCTGAACCTTCCAAAGATGGCTGAAAAAGATGGATGCTTCCAACTGATTCATAGAG 374
 QY 1297 gacacttgctggtgaaaaatcatcactggtcttttggagtttgaggtatcacctagagtag 1356
 Db 375 GAGACTTGCTGCTGTAAGATGGCTGAAAAGATGGATGCTTCCAACTGATTCATAGAGTAC 434
 QY 1357 ctccagaacagatttgagagtagtgaggaaacagccagagcgtgtgcagatgagtagacaaa 1416
 Db 435 CTCAGAACAGATTTGAGAGTAGTGAGGAACAAGCCAGCGAGCTGTGCAGATGAGTACAAAA 494

QY 1417 gtctgtaccagttctctgcagaaaaagcgaagaatctagatgcaataaccaccctcagc 1476
 Db 495 GTCCTGATCCAGTTCTCTGCAGAAAAAGCAAGAATCTAGATGCAATAACCCCTCAGC 554
 QY 1477 ccaaccacaatgcccagcctctgacgaagctgcaggcacagaaccagtggtgctgagagc 1536
 Db 555 CCAACCAACAATGCGCAGCTGCTGACGAAGCTGCAGGCACAGAACCCAGTGGCTGCAGGAC 614
 QY 1537 atgacaactcatctcattctgcgcagctttaaggagttctgcagttccagctcagcgtgagcct 1596
 Db 615 ATGACAACTCATCTCATCTCTGCGCAGCTTTAAGGAGTTCCTGTCAGTCCAGCCTGAGGCT 674
 QY 1597 ctctggcaaatgtagcatgggcaccgtcga 1626
 Db 675 CTTCGGCAAAATGTAGCATGGGCACCTCAGA 704
 RESULT 11
 N80299
 ID N80299 standard; cDNA; 1139 BP.
 AC N80299;
 DT 08-OCT-1990 (first entry)
 DE Interleukin 6.
 KW IL-6; interleukin; cancer; ss.
 FH Key Location/Qualifiers
 FT cds 51..689
 FT /*tag= a
 FT signal_peptide 51..133
 FT /*tag= b
 FT mat_peptide 132..686
 FT /*tag= c
 PN WO8800206-A.
 PD 14-JAN-1988.
 PF 07-JUL-1987; U01611.
 PR 08-JUL-1986; US-883207.
 PA (GENE-) Genetics Inst Inc.
 PI Clark SC, Wong GG, Schendel P, McCoy J;
 DR WPI: 88-021566/03.
 DR P-PSDB; P80269.
 PT Prodn. of non-glycosylated IL-6 - for use in treatment of deficiency
 PT disorders in haematopoietic cells and in cancer therapy.
 PS Disclosure; p; English.
 CC The sequence is carried by pCSF309 in E.coli MC1061 (ATCC 67153) as an
 CC EcoRI insert. It can be excised and used to construct an expression
 CC plasmid for prodn. of IL-6. Bacterially produced IL-6 is non-
 CC glycosylated. It can be used against diseases caused by decreased
 CC levels of either myeloid or lymphoid cells of the haematopoietic system.
 CC It may also be used in conjunction with other interleukin therapies or
 CC as a hybridoma growth factor in culture medium.
 CC See also N80300.
 CC Sequence 1139 BP; 361 A; 240 C; 231 G; 307 T;
 SQ
 Query Match 34.7%; Score 565.2; DB 1; Length 1139;
 Best Local Similarity 99.5%; Pred. No. 1.6e-133;
 Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1057 ccagtagcaccgagagaagattccaaagatgtagccgccccacacagacagccactcacc 1116
 Db 135 CCAGTACCCCGAGAGAAGATTCCAAAGATGTAGCGCGCCCCACACAGACAGCCACTCACC 194
 QY 1117 tcttcagaagaattgacaaacaaattcgggtacatctctcgacggcatctcagccctgaga 1176
 Db 195 TCYTTCAGAACGAATTGACAAACAATTCGGTACATCTCTCAGCGCATCTCAGCCCTGAGA 254
 QY 1177 aaggagacatgtaacagagtaacatgtgtgaaagcagcaaaaggcactggcagaaaaac 1236
 Db 255 AAGGAGACATGTAAACAGAGTAACATGTGTGAAAGCAGCAAAAGGCGACTTGGCAGAAAAAC 314
 QY 1237 aacctgaacctccaagatggctgaaaaagatggatgcttccaattctgattcaatgag 1296
 Db 315 AACCTGAACCTTCCAAAGATGGCTGAAAAAGATGGATGCTTCCAACTGATTCATAGAG 374

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QY 1297 gagacttgcctgggtaaaatcatcactggtcttttggagtttgaggtatcacctagatgac 1356
D 1297 gagacttgcctgggtaaaatcatcactggtcttttggagtttgaggtatcacctagatgac 1356
D 375 GAGACTTGCCTGGTGAAATCATCCTGCTTTTGGAGTTTGAGGTATACCTAGAGTAC 434
QY 1357 ctccagaacagatttgagagtagtgaggaacaaagcagagctgtgcagatgagtagacaaa 1416
D 1357 ctccagaacagatttgagagtagtgaggaacaaagcagagctgtgcagatgagtagacaaa 1416
D 435 CTCCAGAACAGATTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAA 494
QY 1417 gtctgtatccagttcctgcagaaaagcagaagatctagatgcaataaacacccttgac 1476
D 1417 gtctgtatccagttcctgcagaaaagcagaagatctagatgcaataaacacccttgac 1476
D 495 GTCTGTATCCAGTTCTCTGCAGAAAAGCAAGAAATCTAGATGCAATAAACCCCTGAC 554
QY 1477 ccaaccacaaatgccagcctgtgacgaagctgcaggcagacagaaacagtggtgcaggac 1536
D 1477 ccaaccacaaatgccagcctgtgacgaagctgcaggcagacagaaacagtggtgcaggac 1536
D 555 CCAACCAAAATGCCAGCCTGCTGACGAAGCTGCAGGCACAGAACCAAGTGGCTGCAGGAC 614
QY 1537 atgacaactatctcattctgcagcgttttaaggagttcctgcagtcagcctgagggct 1596
D 1537 atgacaactatctcattctgcagcgttttaaggagttcctgcagtcagcctgagggct 1596
D 615 ATGACAACCTCATCTCAATTCCTGCGCAGCTTTAAGGAGTTCTTGCAAGTCCAGCCTGAGGCT 674
QY 1597 ctccgcaaatgtagcagggccacccgtcga 1626
D 1597 ctccgcaaatgtagcagggccacccgtcga 1626
D 675 CTTCGGCAAAATGTAGCATGGGCACCTCAGA 704

RESULT 12
Q01763
ID Q01763 standard; DNA; 1162 BP.
AC Q01763;
DT 27-JUL-1990 (first entry)
DE BSF-2 gene for human B-cell differentiation factor.
KW BSF-2; dhfr; dihydrofolic acid reductase; differentiation.
OS Homo sapiens.
FH Key Location/Qualifiers
FT misc_feature 1..6
FT cds /*tag= a
FT FT 73..708
FT PN J02009388-A.
PD 12-JAN-1990.
PF 8-JUL-1988; 170142.
PR 9-MAR-1988; JP-055270.
PA (AJIN) Ajinomoto KK.
DR WPI; 90-055348/08.
DR P-PSDB; R05415.
DE Physiologically active protein prepn.
PT by transforming plasmid having gene coding physiologically
PT active protein and gene of dihydrofolic acid reductase to hamster
PT ovary etc.
PS Example 3; Fig 6; 12pp; Japanese.
CC Gene may be expressed by transforming a dhfr negative strain of CHO cells
CC with an active BSF-2 gene and dhfr carrying vector. The BSF-2 gene is
CC a B-cell differentiating factor.
SQ Sequence 1162 BP; 359 A; 237 C; 264 G; 302 T;

Query Match 34.7%; Score 565.2; DB 1; Length 1162;
Best Local Similarity 99.5%; Pred. No. 1.6e-133;
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1057 ccagtagccccaggagaagattccaagatgtagccgccccacacagacagccactcacc 1116
D 1057 ccagtagccccaggagaagattccaagatgtagccgccccacacagacagccactcacc 1116
D 157 CCAGTAGCCCCAGGAGAAGATTCCAAAGATGTAGCGCGCCGCCACACAGACGACCTCACC 216
QY 1117 tcttcagaacgaattgacaaaataatcggtacatctcagcggcattctcagccctgaga 1176
D 1117 tcttcagaacgaattgacaaaataatcggtacatctcagcggcattctcagccctgaga 1176
D 217 TCTTCAGAAGAAATGACAAACAAATTCGGTATCTCTCGACGGCATCTCAGCCCTGAGA 276
QY 1177 aaggagacatgtacaagagtaacatgtgtgaagcagcaaaagagcagtggtgcagaaaa 1236
D 1177 aaggagacatgtacaagagtaacatgtgtgaagcagcaaaagagcagtggtgcagaaaa 1236
D 277 AAGGAGACATGTACAAAGAGTAACATGTGTGAAAGCAGCAAAAGAGGCACTGGCAGAAAA 336
QY 1237 aacctgaacctccaagatggctgaaaaagatggatgttccaatctgagttcaatgag 1296
D 1237 aacctgaacctccaagatggctgaaaaagatggatgttccaatctgagttcaatgag 1296

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D 337 AACCTGAACCTTCCAAAGATGGCTGAAAAGATGATGCTTCCAACTTGGATTCAATGAG 396
QY 1297 gagacttgcctgggtaaaatcatcactggtcttttggagtttgaggtatcacctagatgac 1356
D 1297 gagacttgcctgggtaaaatcatcactggtcttttggagtttgaggtatcacctagatgac 1356
D 397 GAGACTTGCCTGGTGAAATCATCCTGCTTTTGGAGTTTGAGGTATACCTAGAGTAC 456
QY 1357 ctccagaacagatttgagagtagtgaggaacaaagcagagctgtgcagatgagtagacaaa 1416
D 1357 ctccagaacagatttgagagtagtgaggaacaaagcagagctgtgcagatgagtagacaaa 1416
D 457 CTCCAGAACAGATTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAA 516
QY 1417 gtctgtatccagttcctgcagaaaagcagaagatctagatgcaataaacacccttgac 1476
D 1417 gtctgtatccagttcctgcagaaaagcagaagatctagatgcaataaacacccttgac 1476
D 517 GTCTGTATCCAGTTCTCTGCAGAAAAGCAAGAAATCTAGATGCAATAAACCCCTGAC 576
QY 1477 ccaaccacaaatgccagcctgtgacgaagctgcaggcagacagaaacagtggtgcaggac 1536
D 1477 ccaaccacaaatgccagcctgtgacgaagctgcaggcagacagaaacagtggtgcaggac 1536
D 577 CCAACCAAAATGCCAGCCTGCTGACGAAGCTGCAGGCACAGAACCAAGTGGCTGCAGGAC 636
QY 1537 atgacaactatctcattctgcagcgttttaaggagttcctgcagtcagcctgagggct 1596
D 1537 atgacaactatctcattctgcagcgttttaaggagttcctgcagtcagcctgagggct 1596
D 637 ATGACAACCTCATCTCAATTCCTGCGCAGCTTTAAGGAGTTCTTGCAAGTCCAGCCTGAGGCT 696
QY 1597 ctccgcaaatgtagcagggccacccgtcga 1626
D 1597 ctccgcaaatgtagcagggccacccgtcga 1626
D 697 CTTCGGCAAAATGTAGCATGGGCACCTCAGA 726

RESULT 13
N90131
ID N90131 standard; DNA; 1101 BP.
AC N90131;
DT 1-NOV-1989 (first entry)
DE DNA sequence of pBSF2-L8
KW pBSF2-L8; pGEM4; cDNA; clone; Fc epsilon R-gene; IgE; allergy.
FH Key Location/Qualifiers
FT misc_feature 1..6
FT cds /*tag= a
FT FT 7..642
FT FT /*tag= b
FT FT misc_feature 1097..1101
FT FT /*tag= c
PN EP-321842-A.
PD 28-JUN-1989.
PF 14-DEC-1988; 120878.
PR 22-DEC-1987; EP-100814.
PA (OSAU) Osaka University.
PI Kishimoto T, Suemura M, Kikutani H, Barsumian EL, Schneider FJ;
DR WPI; 89-186249/26.
DR P-PSDB; P90047.
DE Cloned gene for eukaryotic expression of Fc epsilon receptor
PT - for use in treatment and prophylaxis of allergy, resp. asthma.
PS Disclosure; fig 3; 24pp; English.
CC pBSF2-L8 is prep'd. by digesting pBSF-2.38 with HindIII and BamHI
CC to obtain a 1.2 kbp EcoRI-BamHI BSF-2 cDNA insert. This was digested
CC with HinfI, end-filled, and digested with KpnI. A 100 bp
CC KpnI-HinfI fragment contg. BSF-2 leader sequence was cloned into
CC the multiple cloning site of KpnI-SmaI digested pGEM4, and one of the
CC selected clones named as pBSF2-L8. It is used in prepn. of pSFC
CC epsilon R-1 (see N90132). The misc. feature a is a KpnI site, and
CC c is a BamHI site. The encoded peptide sequence (see P90047) includes
CC that of the BSF-2 signal sequence.
SQ Sequence 1101 BP; 351 A; 227 C; 224 G; 299 T;

Query Match 34.6%; Score 563.6; DB 1; Length 1101;
Best Local Similarity 99.3%; Pred. No. 4e-133;
Matches 566; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1057 ccagtagccccaggagaagattccaagatgtagccgccccacacagacagccactcacc 1116
D 1057 ccagtagccccaggagaagattccaagatgtagccgccccacacagacagccactcacc 1116
D 91 CCAGTAGCCCCAGGAGAAGATTCCAAAGATGTAGCGCGCCGCCACACAGACGACCTCACC 150
QY 1117 tcttcagaacgaattgacaaaataatcggtacatctcagcggcattctcagccctgaga 1176

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Db 151 TCTTCAGAGCAATTCACAAACAAATTCGGTACATCTCGACGGCATCTCAGCCCTGAGA 210
QY 1177 aaggagacatgtacaagagtaacatgtgtgaaagcagacaaagcagcactggcagaaaaac 1236
Db 211 AAGGAGACATGTAAACAGAGTAACATGTGTGAAAGCAGACAAAGAGGCACCTGGCAGAAAAAC 270
QY 1237 aacctgaaccttccaagatggctgaaaaagatggatgcttccaatctgattcaatgag 1296
Db 271 AACCTGAACCTTCCAAGATGGCTGAAAAAGATGGATGCTTCCAATCTGGATTCAATGAG 330
QY 1297 gagaactgctgggtgaaatcatcactggtctcttttggagtttgaggtatataccttagagtac 1356
Db 331 GAGACTTGGCTGGTGAATAATCATCACTGGTCTCTTTGGAGTTTGAGGTATACCTTAGAGTAC 390
QY 1357 ctccagaacagattgagagtagtgaggaacagcagagctgtgcagatgagtcagacaaaa 1416
Db 391 CTCAGAACAGATTTGAGAGTAGTGAGGAACAGCCAGAGCTGTGCAGATGAGTACAAAA 450
QY 1417 gtctgatccagttctgcagaaaaaggcaagaatctagatgcaataaacacccctgac 1476
Db 451 GTCTGATCCAGTTCCTGCAGAAAAAGGCAAGAAATCTAGATGCAATAACCAACCCCTGAC 510
QY 1477 caaacacaaaatgcagcctgtgcagaaagctgcaggcacagaaccagtggtgcaggac 1536
Db 511 CCAACACACAAATGCCAGCCTGCTGACGAAGCTGCAGGCACAGAACCAAGTGGCTGCAGGAC 570
QY 1537 atgacaactcatctcttcgcagcctttaaggagttctcagtcagtcacccctgagggct 1596
Db 571 ATGACAACTCACTCAATCTGCGCACCTTTAAGGAGTTCCTGCAAGTTCAGCCCTGAGGGCT 630
QY 1597 ctccgcaaatgtagcatgggaccctcga 1626
Db 631 CTTCCGCAAAATGTAGCATGGCACCCTCAGA 660

RESULT 14
N90135
ID N90135 standard; DNA; 1101 BP.
AC N90135;
DT 1-NOV-1989 (first entry)
DE DNA sequence of pBSF2-L8
KW Fc epsilon receptor; cloned gene; IgE; pBSF2-L8; allergy; asthma; BSF-2.
FH Key Location/Qualifiers
FT misc_feature 2..5
FT cds /*tag= a
FT /*tag= b
FT misc_feature 1097..1101
FT /*tag= c
EP-321601-A.
PD 28-JUN-1989.
PF 22-DEC-1987; 119080.
PR 22-DEC-1987; EP-119080.
PI (OSAU) Osaka University
PA Kishimoto T, Suemura M, Kikutani H, Barsumian E;
DR WPI; 89-186101/26.
DR P-PSDB; P90371.
PT Cloned genes coding for soluble IgE receptor - comprising modified coding
PT sequence of Fc epsilon receptor gene.
PS Disclosure; fig. 3; 20pp; English.
CC Sequence of pBSF2-L8, which is used as a vector in prepn. of plasmid
CC pFc epsilon R-1. It is prepd. by inserting BSF-2 cDNA insert (from
CC BSF-2.38) into pGEM4. Misc. feature a is a KpnI site, and c is a BamHI
CC site. See also N90134, N90136 and P90371 for encoded peptide.
SQ Sequence 1101 BP; 351 A; 227 C; 224 G; 299 T;

Query Match 34.6%; Score 563.6; DB 1; Length 1101;
Best Local Similarity 99.3%; Pred. No. 4e-133;
Matches 566; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1057 ccagtaacccccaggagaagatctcaaaagatgtagcgcgccccacacagacagccactcacc 1116

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Db 91 CCAGTACCCCCAGGAGAAATTCCAAAGATGTAGCCGCCACACAGACAGCCACTCACC 150
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RESULT 15
N90345
ID N90345 standard; DNA; 1101 BP.
AC N90345;
DT 1-NOV-1989 (first entry)
DE Plasmid pBSF2-L8, encoding whole human lymphocyte receptor
DE for immunoglobulin
KW Human lymphocyte receptor for immunoglobulin; cDNA;
KW eukaryotic signal sequence; hypersensitivity; allergy; asthma;
KW BSF-2 leader sequence; plasmid pFc-epsilon-R-1; immunoglobulin E.
OS Homo sapiens (Human)
FH Key Location/Qualifiers
FT /*tag= a
FT EP-324879-A.
PD 26-JUL-1989.
PF 20-JAN-1988; 100814.
PR 20-JAN-1988; EP-100814.
PA (KISH) Kishimoto T.
PI Schwenkenwein R, Sommergruber W, Swetly P;
DR WPI; 89-214148/30.
DR P-PSDB; P90121.
PT Soluble recombinant Fc-epsilon receptor
PT - used for treatment or prophylaxis of local and
PT allergic reactions induced by IgE.
PS Disclosure; fig 3; 24pp; English.
CC Plasmid pBSF2-L8, encoding whole human lymphocyte receptor
CC for immunoglobulin (see p90121). Has BSF-2 leader sequence
CC (c.f. N90344). Used to produce highly bioactive
CC water-soluble FcR. Pref. has interleukin signal sequence.
CC Water-soluble FcR binds IgE, so it is useful for treating
CC hypersensitivity, esp. asthma.
SQ Sequence 1101 BP; 351 A; 227 C; 224 G; 299 T;

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Query Match		34.6%	Score 563.6;	DB 1;	Length 1101;	
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2000, 13:48:06 ; Search time 2865.12 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 972840 seqs, 892348106 residues 1945680
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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82: gb_v12.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	995	61.2	2087	5	E02673	E02673 CDNA encodi
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16	565.2	34.7	1113	11	HUMIL6CSF	M54894 Human inter
17	565.2	34.7	1125	9	HUMIFNB2B	M18403 Human hybri
18	565.2	34.7	1139	5	I08633	I08633 Sequence 2
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DEFINITION Sequence 2 from Patent WO9732891.
ACCESSION A93715
VERSION A93715.1 GI:6741887
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1612)
AUTHORS Rose-John,S.
TITLE CONJUGATE FOR MODIFYING INTERACTIONS BETWEEN PROTEINS
JOURNAL Patent: WO 9732891-A 12-SEP-1997;
ANGEWANDTE GENTECHNOLOGIE SYST (DE); ROSE JOHN STEFAN (DE)
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VERSION	E04823.1	GI:2173019	
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ORGANISM	Homo sapiens		
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AUTHORS	Kishimoto,C., Hachiman,H. and Yasukawa,K.		
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Qy	608	tgtcgctgcagtagtgctcgaggagcaagttcagcaaaactcaaaccttttcaggggtgtg	667
Db	800	TGTGGTGCAGTAGTGTTCGGGACAAAGTTTCAGCAAAACTCAAACCTTTCAGGGTTGTG	859
Qy	668	gaatttgcagctgataccgctgcacacatcaacagtcactgcggtggcagaacaccccc	727
Db	860	GAATCTTGACGCTGATCCGCTGCCAATCATCAGTCACTGCCGTGGCCAGAACCCCC	919
Qy	728	gctggtcagtgctcaactggaacacccccactcctggaactcatcttctcacagactac	787
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Qy	788	ggtttgagctcagatatacggtgaacggtcaagacattcacacatggtatggtcaagg	847

Db 980 GGTGGAGTCAGATATACGGCTCAACGGTCAAGACATTCACAACATGGATGGTCAAGG 1039
 QY 848 acctcagcatcactgtgtcattccacgacgctgagcgccctgagcgacgtggtgacgc 907
 Db 1040 ACTCCAGCATCAGTGTGTATCCACGAGCCTTGAGCGCCCTGAGCACGTTGGTGCACG 1099
 QY 908 ttctgtccacgagagaggttcgggcaaggcgagtgagcagtgagcggcgagggccatgg 967
 Db 1100 TTCTGTCCCGCAGGAGGAGTTCGGGCAAGCGAGTGGAGCGAGTGGAGCCCGGAGGCCATGG 1159
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 Db 1160 GCACGCCCTTGGACAGAAATCCAGGAGTCTCTCCAGCT 1194

 RESULT 4
 E02673 2087 bp RNA PAT 29-SEP-1997
 LOCUS CDNA encoding human B cell stimulating factor 2 receptor protein.
 DEFINITION E02673
 ACCESSION E02673
 VERSION E02673.1 GI:2170901
 KEYWORDS JP 1990288898-A/1.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 2087)
 Kishimoto,C.
 HUMAN B CELL STIMULATION FACTOR 2 RECEPTOR PROTEIN
 TITLE Patent: JP 1990288898-A 1 28-NOV-1990;
 JOURNAL KISHIMOTO CHUZO
 COMMENT OS Homo sapiens (human)
 PN JP 1990288898-A/1
 PD 28-NOV-1990
 PF 20-JAN-1989 JP 1989009774
 PR 22-JAN-1988 JP 88P 12387, 25-JAN-1988 JP 88P 12599, PR
 04-AUG-1988 JP 88P 194885, 14-JAN-1989 JP 89P 7461 PI
 KISHIMOTO CHUZO
 PC C07K15/06,C07K13/00,C12N5/10,C12N5/20,C12N15/19,C12N15/85, PC
 C12P21/02
 PC C12P21/08/A61K37/02,A61K37/02,A61K39/395,C12N15/06,
 C12P21/02,
 PC C12R1:91),(C12P21/08,C12R1:91);
 CC strandedness: Double;
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 CC hypothetical: No;
 CC anti-sense: No;
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 CC *source: cell_line=YT;
 CC *source: clone=PIB1SP2R;
 FH key Location/Qualifiers
 FH CDS
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 FT receptor
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 FT Location/Qualifiers
 FT 1..2087
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 FT /db_xref='taxon:9606'
 BASE COUNT 425 a 645 c 623 g 394 t
 ORIGIN

Query Match 61.2%; Score 995; DB 5; Length 2087;

Best Local Similarity 100.0%; Pred. No. 3.6e-225;

Matches 995; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 catgagtgtagcgcgagaggaagcatgctgcccctggctgcgcgtgcgcgtgcgcgcgcgc 67
 Db 221 CATGAGTGTGATGCCGAGGAGGAAGCATGCTGGCCCTGGCTGGCTGGCTGGCTGGCTGGCC 280
 QY 68 tctgtgcccgc 127
 Db 281 TGCTGGCCCGCGCGGAGCGCGCTGGCCCAAGGCGCTGCCCTGGCGCAGGAGGTGGCAA 340
 QY 128 gagcgtgctgaccagctgcccagagagacagcgtgactctgacctgcccgggggtagagc 187
 Db 341 GAGGGGTGCTGACCACTGTGCCAGGAGACAGCGTACTCTGACCTGCCCGGGGGTAGAGC 400
 QY 188 cggaaagacaatgccactgttcaactggtgctcaggaagccgctcagcagctcccccaccca 247
 Db 401 CGGAAGACAAATGCCACTGTTCACTGGGTGCTCAGGAAGCCGGCTGCAGGCTCCACCCCA 460
 QY 248 gcagatgggtggcctgggaaggaggtgctgctgaggtcggtgcagctccacgactctg 307
 Db 461 GCAGATGGGTGGCATGGGAAGGAGGCTGCTGCTAGGTGGGTGAGCTCCAGCACTCTG 520
 QY 308 gaaactattcagtctaccggcgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 367
 Db 521 GAAACTATTTCATGCTACCGGGCGCGCCAGCTGGGACTGTGCACTTGTCTGGTGGATG 580
 QY 368 ttccccccgagagcccgagctctcctgcttcgcgaagagcccccctcagcaatgtgttt 427
 Db 581 TTCCCCCGGAGGAGGCCCGAGCTCTCTGCTCCGGGAAGAGCCCCCTCAGCAATGTGTGT 640
 QY 428 gtgagtgggtgctcctggagcaccctccctcctcagcaaaaggctgctcttggtagga 487
 Db 641 GTGAGTGGGTCTCTCGAGACCCCATCTCTGACGACAAAGAGCTGTGCTTGGTGAGGA 700
 QY 488 agtttcagaagacgtccgc 547
 Db 701 AGTTTCAGAACAGTCCGCGCGAAGACTTTCAGAGAGCCGTGCCAGTATTCACAGGAGTCCC 760
 QY 548 aqaagtctctcctgcagtttagcagtcctccggagggagagcagctcttctacatagtcca 607
 Db 761 AGAAGTTCTCTCTGCCAGTTAGCAGTCCCGGAGGAGACAGCTCTTCTACATAGTGTCCA 820
 QY 608 tctgcgtccagtagtgctggggagcaagtctcagcaaaactcaaaccttccaggggtgtg 667
 Db 821 TGTGGGTGCCAGTAGTGTGGGAGCAAGTTTCAGCAAAAACCTCAAACCTTTCAGGGTGTG 880
 QY 668 gaatttcagcagcctgacccgc 727
 Db 881 GAATCTTGACGCTGATCCGCTGCCAACATCACAGTCACTGCCGTGGCCAGAAACCCCC 940
 QY 728 gctggctcagtgctcactggcgaagacccccactcctgggaactcattcttctacagactac 787
 Db 941 GCTGGCTCAGTGTCACTGGCAAGACCCCACTCTCTGGAACTCATCTTCTACAGACTAC 1000
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 RESULT 5
 E12979
 LOCUS E12979 3319 bp DNA PAT 24-JUN-1998
 DEFINITION CDNA encoding human interleukin-6 receptor.

*	29626	30425:	gap of	800 bp	
*	30426	37201:	contig of	6776 bp in length	
*	37202	38001:	gap of	800 bp	
*	38002	39518:	contig of	1517 bp in length	
*	39519	40318:	gap of	800 bp	
*	40319	52258:	contig of	11940 bp in length	
*	52259	53058:	gap of	800 bp	
*	53059	56384:	contig of	3326 bp in length	
*	56385	57184:	gap of	800 bp	
*	57185	92891:	contig of	35707 bp in length	
*	92892	93691:	gap of	800 bp	
*	93693	97942:	contig of	4251 bp in length	
*	97943	98742:	gap of	800 bp	
*	98743	116105:	contig of	17363 bp in length	
*	116106	116905:	gap of	800 bp	
*	116906	119375:	contig of	2470 bp in length	
*	119376	120175:	gap of	800 bp	
*	120176	134110:	contig of	13935 bp in length	
*	134111	134910:	gap of	800 bp	
*	134911	146286:	contig of	11376 bp in length	
*	146287	147086:	gap of	800 bp	
*	147087	163093:	contig of	16007 bp in length	
*	163094	163893:	gap of	800 bp	
*	163894	168372:	contig of	4479 bp in length.	

FEATURES	SOURCE
1. Feature 1	Source 1
2. Feature 2	Source 2
3. Feature 3	Source 3
4. Feature 4	Source 4
5. Feature 5	Source 5
6. Feature 6	Source 6
7. Feature 7	Source 7
8. Feature 8	Source 8
9. Feature 9	Source 9
10. Feature 10	Source 10

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/chromosome="9"
/map="q21.33-22.2"
/clone="RP11-406A20"
/clone_lib="PBC1-112"
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BASE COUNT	44685 a	34503 c	34478 g	43492 t	11214 others
ORIGIN					

Query Match	35.58;	Score 577.8;	DB 40;	Length 168372;
Best Local Similarity	77.74;	Pred. No. 2.1e-126;		
Matches 773;	Conservative 0;	Mismatches 192;	Indels 30;	Gaps 5;
Qy	8	catgagtggtagccgaggaggaacatgctggccgtgcgtgcgtgcgtgcgtgcgtgcgc	67	
Db	67573	CAC TGGG CATTAG CCAAG AAGACATGCTGGCCATCAGCTGAGTGTGCTGCCACAC	67632	
Qy	68	tgctggccgcgcgggagcgctggccccaaggcgtgccttcgcgcagaggtggca	127	
Db	67633	TGCGGGCAGTCTG-----CCCAAGAGGCTGCCCTACGCTGGAGGCAGTGA	67679	
Qy	128	gagcgctgctgaccagctctgcagagagacgcgtgactctgacctgcccggggtagagc	187	
Db	67680	GTGATGTGCTGA-----CCAGGATACTGCATTCCTCCCTGACCTGTCCAGAGGGAAC	67731	
Qy	188	cggaaagacattgccactttcactgggtgcgtcagaaacccgctgcaggtcccccacca	247	
Db	67732	CTGAAATTCATGCCACTGTCCACTGGTTGCACAGGACTCCACGCCAGGCTACGCCCCA	67791	
Qy	248	gcagatggctggcatgggaaagaggtgctgctgagctcgtgcagctccacgactctg	307	
Db	67792	CGAGATGGCTGGTCTGGAGGAGGCTGCTTCTCAGGTGGTGCAGCTCTCGCACTCTG	67851	
Qy	308	gaacctattcatgctaccgggcccggcccccagctggagactgacattgctggatg	367	
Db	67852	GAAACTATTCTGCTGCCGGGTGGCTGCCACAGG---TCTGTGCTGTGTTGGTGGATG	67909	
Qy	368	ttcccccgaggagccccagctctcctctccgaagagccccctcaagaattgttgtt	427	
Db	67910	TTTCTCCGTGAGGAGCTCAGCTCTCCTGCTCTTGAAGAGCCCCCTCAGTGACATTGGTT	67969	
Qy	428	gtgagtggggtcctcgagacaccccccatccctgacgacaaaggtgctgcttggtagga	487	
Db	67970	GTGATAGAGTCTTGGAGTCAAGGTTCTGAGTC----AAAGCTGTGCTATTGCTGAGAA	68025	
Qy	488	agtttcgaacacagtcggccggaagacttccaggagccgtgcagattatccccaggatccc	547	

[illegible]

RESULT 13

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LOCUS       HSILB2R      1098 bp      mRNA                      PRI      21-MAR-1995
DEFINITION  Human mRNA for interleukin BSF-2 (B-cell differentiation factor).
ACCESSION   X04602
VERSION     X04602.1  GI:33849
KEYWORDS    B-cell differentiation factor; interleukin BSF-2; signal peptide.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE   1 (bases 1 to 1098)
AUTHORS     Hirano,T., Yasukawa,K., Harada,H., Taga,T., Watanabe,Y.,
            Matsuda,T., Kashiwamura,S.I., Nakajima,K., Koyama,K., Iwamatsu,A.,
            Tsunasawa,S., Sakiyama,F., Matsui,H., Takahara,Y., Taniguchi,T. and
            Kishimoto,T.
TITLE        Complementary DNA for a novel human interleukin (BSF-2) that
            induces B lymphocytes to produce immunoglobulin
JOURNAL     Nature 324 (6092), 73-76 (1986)
MEDLINE     87065033
FEATURES     Location/Qualifiers
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CDS

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Best Local Similarity 99.5%; Pred. No. 1.8e-123;
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1117 tcttcagaacgaattgacaaacaaatctcggtacatctcgagcgcatctcagccctgaga 1176
DB 178 TCTTCAGAACGAATTGACAAACAAATTCGGTACATCTCGAGCGCATCTCAGCCCTGAGA 237

QY 1177 aaggagacatgtaacagagtaacatgtgtgaagcagcaagagagcactggcagaaaaac 1236
DB 238 AAGGAGACATGTAAACAGAGTAAATGTGTGAAGCAGCAAGAGGCACTGGCAGAAAAAC 297

QY 1237 aaactgaaccttcacaaagatggtgtaaaagatggatgttccaatctggattcaatgag 1296
DB 298 AACCTGAACCTTCCAAAGATGGCTGAAAGATGGATGCTTCCAATCTGGATTCAATGAG 357

QY 1297 gagacttgctggtaaaatcatcactggtcttttgagatttgaggatatacctagagtagc 1356
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QY 1357 ctccagaacagatttgagagtagtgaggaacagcagagctgtgcagatgagtagacaaa 1416
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QY 1417 gtctgattccagttctgcagaaaaaggcaaaagatcttagatgcaataaccacccctgac 1476
DB 478 GTCTGTATGCATTCCTGCAGAAAAAGGCAAAAGATCTAGATGCAATAACCAACCCCTGAC 537

QY 1477 caaacacaaaatgcagcctgtgcagaaagctgcaggcagcaaacagctggctgcaggac 1536
DB 538 CCAACACAAAATGCCAGCCTGTCTGACGAAGCTGCAGGCACAGAACCCAGTGGCTGCAGGAC 597

QY 1537 atgacaactcatctattctgcagcctttaaggagttcttcagctccagcctgaggct 1596
DB 598 ATGACAACTCATCTATTCTGGCAGCTTTAAGGAGTTCTCGAGTTCCTCGAGTCCAGCTGAGGGCT 657

QY 1597 cttcggaatgtagcatgggcaccgtcga 1626
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LOCUS      E03737      1102 bp      RNA      PAT      29-SEP-1997
DEFINITION cdna encoding human B-cell differentiation factor.
ACCESSION  E03737
VERSION    E03737.1 GI:2171952
KEYWORDS  JP 1992169599-A/1.
SOURCE    Homo sapiens.
          ORGANISM
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 1102)
AUTHORS   Yasueda,H., Nagase,K., Kawai,M., Fukuhara,K. and Matsui,Y.
TITLE     VARIANT HUMAN BCDF

JOURNAL Patent: JP 1992169599-A 1 17-JUN-1992;
COMMENT AJINOMOTO CO INC
PN OS Homo sapiens (human)
PD JP 1992169599-A/1
PF 17-JUN-1992
PP 30-OCT-1990 JP 1990290704
PI YASUEDA HISASHI, NAGASE KAZUO, KAWAI MISAOKO, FUKUHARA KENICHI,
PM MATSUI YUTAKA
PC C07K13/00,C12N15/24,C12P21/02,/A61K37/02,A61K37/02,A61K37/02,
PC (C12P21/02,
PC C12R1:19);
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CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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BASE COUNT 336 a 238 c 226 g 302 t
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Query Match      34.7%; Score 565.2; DB 5; Length 1102;
Best Local Similarity 99.5%; Pred. No. 1.8e-123;
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1057 ccagtaaccccgaggagaattccaaagatgtagccgccccacacagacagccactcacc 1116
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QY 1117 tcttcagaacgaattgacaaacaaatctcggtacatcttcctgcagcgcatctcagccctgaga 1176
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QY 1357 ctccagaacagatttgagagtagtgaggaaacagccagagctgtgcagatgagtagacaaa 1416
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QY 1477 ccaaacacaaaatgccagcctgtgcagaaagctgcagcagcagacacagctggctgcaggac 1536
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QY 1537 atgacaactcatctattctgcagcctttaaggagttcttcagctccagcctgaggct 1596
DB 600 ATGACAACCTCATCTCATTTCTGCGCAGCTTTAAGGAGTTCTTCGAGTCCAGCTCAGGGCT 659
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Run on: Thu Aug 10 16:03:23 2000; MasPar time 40.32 Seconds
Tabular output not generated. 902.719 Million cell updates/sec

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Perfect Score: 3803
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Scoring table: PAM 150
Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrcm112
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5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 50.204; Variance 95.919; scale 0.523

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1320	34.7	440	11	INTERLEUKIN 6 RECEPTOR	3.24e-249
2	1239	32.6	209	6	INTERLEUKIN-6 (FRAGMENT)	1.69e-231
3	814	21.4	209	6	INTERLEUKIN 6 (FRAGMENT)	1.71e-139
4	810	21.3	205	6	INTERLEUKIN 6 (FRAGMENT)	1.23e-138
5	804	21.1	208	6	INTERLEUKIN 6 (FRAGMENT)	2.35e-137
6	748	19.7	160	6	INTERLEUKIN-6 (FRAGMENT)	2.04e-125
7	725	19.1	207	6	INTERLEUKIN 6 (FRAGMENT)	1.57e-120
8	539	14.2	210	11	IL-6 (FRAGMENT)	1.71e-81
9	413	10.9	372	11	CILIARY NEUTROTROPHIC F	9.20e-56
10	401	10.5	432	11	INTERLEUKIN-11 RECEPTOR	2.34e-53
11	400	10.5	432	11	INTERLEUKIN-11 RECEPTOR	3.71e-53
12	397	10.4	66	6	INTERLEUKIN 6 RECEPTOR	1.48e-52
13	381	10.0	94	6	INTERLEUKIN 6 (FRAGMENT)	2.28e-49
14	377	9.9	422	4	INTERLEUKIN-11 RECEPTOR	1.42e-48
15	329	8.7	101	11	INTERLEUKIN 6 (FRAGMENT)	3.77e-39
16	252	6.6	204	14	ORF K2.	1.50e-24
17	252	6.6	204	14	INTERLEUKIN-6 HOMOLOG	1.50e-24
18	205	5.4	422	4	CYTOKINE-LIKE FACTOR-1	4.14e-16
19	182	4.8	228	11	CYTOKINE RECEPTOR-LIKE	3.59e-12
20	179	4.7	296	6	PROLACTIN RECEPTOR SHO	1.14e-11

21 180 4.7 581 6 046561 PROLACTIN RECEPTOR LON 7.76e-12
22 168 4.4 229 4 075269 HUMAN CYTOKINE RECEPTO 7.44e-10
23 163 4.3 229 4 014213 CYTOKINE RECEPTOR PREC 4.80e-09
24 161 4.2 346 13 093404 PROLACTIN RECEPTOR (FR 1.01e-08
25 154 4.0 316 11 035545 INTRON 5-INSERTED FORM 1.30e-07
26 151 4.0 335 6 079203 PROLACTIN RECEPTOR (FR 3.84e-07
27 142 3.7 206 4 016354 PROLACTIN RECEPTOR (FR 9.28e-06
28 130 3.4 217 6 046386 PROLACTIN RECEPTOR (FR 5.57e-04
29 130 3.4 329 6 09XS05 INTERLEUKIN 12 P40 SUB 5.57e-04
30 130 3.4 625 6 09XS52 PROLACTIN RECEPTOR PRE 5.57e-04
31 129 3.4 895 11 062960 LEPTIN RECEPTOR. 7.77e-04
32 124 3.3 194 6 002708 GRANULOCYTE COLONY-STI 4.01e-03
33 124 3.3 229 6 027950 ERYTHROPOIETIN RECEPTO 4.01e-03
34 124 3.3 229 6 028206 ERYTHROPOIETIN RECEPTO 4.01e-03
35 124 3.3 344 13 042403 ATTACHMENT REGION BIND 4.01e-03
36 125 3.3 471 11 09WTN9 MRNA, COMPLETE CDS, SI 2.89e-03
37 126 3.3 874 11 093737 INTERLEUKIN 12 RECEPTO 2.09e-03
38 125 3.3 1084 10 043010 SUCROSE PHOSPHATE SYNT 2.89e-03
39 121 3.2 313 5 077284 BEADUX/DLMO PROTEIN. 1.05e-02
40 121 3.2 738 5 002402 INSOLUBLE PROTEIN. 1.05e-02
41 122 3.2 862 4 099665 IL-12 RECEPTOR BETA2. 7.64e-03
42 122 3.2 881 13 057519 GPI30PL. 7.64e-03
43 123 3.2 1165 6 002671 TRANSMEMBRANE LEPTIN R 5.54e-03
44 121 3.2 1571 4 060469 DOWN SYNDROME CELL ADH 1.05e-02
45 121 3.2 1896 4 060468 DOWN SYNDROME CELL ADH 1.05e-02

ALIGNMENTS

RESULT 1
ID Q00343 PRELIMINARY; PRT; 440 AA.
AC Q00343;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE INTERLEUKIN 6 RECEPTOR, ALPHA PRECURSOR
DE (MUTANT INTERLEUKIN-6 RECEPTOR).
GN IL6RA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE: 90278354.
RA SUGITA T., TOTSUKA T., SAITO M., YAMASAKI K., TAGA T., HIRANO T.,
RA KISHIMOTO T.;
RT "Functional murine interleukin 6 receptor with the intracisternal A
RT particle gene product at its cytoplasmic domain. Its possible role in
RT plasmacytomagenesis."
RL J. Exp. Med. 171:2001-2009(1990).
CC -1- MISCELLANEOUS: THIS PROTEIN IS A ABNORMAL INTERLEUKIN-6 RECEPTOR.
CC IN THE CDNA ENCODING THE ABNORMAL INTERLEUKIN-6 RECEPTOR THE
CC REGION CORRESPONDING TO ITS INTRACYTOPLASMIC DOMAIN WAS REPLACED
CC WITH A LONG TERMINAL REPEAT OF THE INTRACISTERNAL A PARTICLE (IAP)
CC GENE. A MEMBER OF THE ENDOGENOUS PRORETROVIRAL-LIKE ELEMENTS
CC PRESENT IN THE GENOME OF MUS MUSCULUS.
DR EMBL: X51976; CAA36238.1;
DR PIR: JLO144; JLO144.
DR HSSP: P14787; IAN3.
DR MGD: MGI:105304; IL6ra.
DR PFAM: PF00041; fn3; 1.
DR PFAM: PF00047; i9; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT CHAIN 1 19
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[illegible][illegible]

	Query Match	32.6%	Score 1239;	DB 6;	Length 209;
	Best Local Similarity	97.2%;	Pred. No. 1.69e-231;		
	Matches 176;	Conservative	Mismatches 0;	Indels 0;	Gaps 0;
Db	29	PVPGEDSKVAARNROPLTSTEODIKHRIYILDGISALRKETCKKNMCESSKEALAE	88		
Qy	342	PVPGEDSKDVAARNROPLTSSRIDKQIRYILDGISALRKETCKKNMCESSKEALAE	401		
Db	89	NLNP.KMAEKDGCQFSGFNEETCLVKITITGLLEFEVLYLQNFESSEQARAVOMSTK	148		
Qy	402	NLNP.KMAEKDGCQFSGFNEETCLVKITITGLLEFEVLYLQNFESSEQARAVOMSTK	461		
Db	149	VLIQFLOKKAKNLDATITPPDPTTNASLLTKLOAQONQWLDQMTTHILIRSKFEFLQSSLR	208		
Qy	462	VLIQFLOKKAKNLDATITPPDPTTNASLLTKLOAQONQWLDQMTTHILIRSKFEFLQSSLR	521		

[illegible]

Query Match	21.4%	Score 814;	DB 6;	Length 209;
Best Local Similarity	59.2%;	Pred. No. 1.71e-139;		
Matches	109;	Conservative	35;	Mismatches 40; Indels 0; Gaps 4
Db	26	PGVGGESQADATSNRPPLTSPDKMBEEFKYILGRISALRKEMCDKYKNKCEDSKAALAE	85	
Qy	342	PVPPGEDSKDVAAPHQPLTSSERIDKQRYILDGISALRKETCNKSNWCESSKEALAE	401	
Db	86	NLRPLKLAEKDGGCFQSGFNOETCLRIITGLLEFQIHUKYQANVEGKNEDANSVYIS	145	
Qy	402	NLNLPKMAEYDGGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFPESSEQARAVQ	461	
Db	146	LLVQMLMKYKVSODEVYTPDPPTDTSLOAILKADOKWLKHTTHILHLSRLEDFLO	205	
Qy	462	VLQFLOQKAKNLDATTPDPPTNALLTKLQAQNWQLODMTHILLRSPKEFLQSS	521	
Db	206	VRIM	209	
Qy	522	LROM	525	

RESULT	4	PRELIMINARY;	PRT;	205 AA.
ID	Q28747			
AC	Q28747;			
DT	01-NOV-1996 (TReMBLrel. 01, Created)			
DT	01-NOV-1996 (TReMBLrel. 01, Last sequence update)			
DT	01-NOV-1999 (TReMBLrel. 12, Last annotation update)			
DE	INTERLEUKIN 6 (FRAGMENT).			
GN	IL-6.			
OS	Orcinus orca (Killer whale).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
NC	Euthera; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae; Orcinus.			
RC	[1]			
RR	SEQUENCE FROM N.A.			
RP	MEDLINE: 96163018.			
RX				
RA	KING D.P., SCHRENZEL M.D., MCKNIGHT M.L., REIDARSON T.H., HANNI K.D.,			
RA	STOTT J.L., FERRICEL D.A.;			
RT	"Molecular cloning and sequencing of interleukin 6 cDNA fragments from			
RT	the harbor seal (<i>Phoca vitulina</i>), killer whale (<i>Orcinus orca</i>), and			
RT	southern sea otter (<i>Enhydra lutris nereis</i>).";			

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RL Immunogenetics 43:190-195(1996).
DR EMBL; I46803; AAB01429.1; -.
DR HSSP; P05231; 1ALU.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR PFAM; PF00489; IL-6; 1.
FT NON_TER 1
SQ SEQUENCE 205 AA; 23266 MW; C853C8DF CRC32;

Query Match 21.3%; Score 810; DB 6; Length 205;
Best Local Similarity 60.7%; Pred. No. 1.23e-138;
Matches 111; Conservative 36; Mismatches 35; Indels 1; Gaps 1;

Db 21 PGPLGDFKDDTSDRLTSPDKTEALIKYILGKISAMRKCEKYDKCNSKEALAEN 80
QY 342 PVPPGDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKETCNKSNMCESSKEALAEN 401
Db 81 NLNPKMAEKDGCFCGSGFNOETCLMRITTCGLLEYQIYLDYQNEYEGDKAEIAVQISSK 140
QY 402 NLNPKMAEKDGCFCGSGFNEETCLVKITGLLEFEVYLEYLNRFESSEEQARAVQMSTK 461
Db 141 ALAQILRQKVKNPDEVTTDPPTTNASIMNMQSONDDMKNTKIILRLSLENFLQFSLR 200
QY 462 VLIOFLQKRAKNLDAITDPPTTNASILLKLOAQNO-WLQDWTTHLLRSFKFLOSSLR 520
Db 201 AIR 203
QY 521 ALR 523

RESULT 5
ID Q9XTR80 PRELIMINARY; PRT; 208 AA.
AC Q9XTR80;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE INTERLEUKIN 6 PRECURSOR.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Monodontidae;
OC Delphinapterus.
RN [1]
RP SEQUENCE FROM N.A.
RA ST-LAURENT G., DE GUISE S., FOURNIER M., ARCHAMBAULT D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) interleukin 6."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076643; AAD42929.1; -.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 208 AA; 23456 MW; 0FA70646 CRC32;

Query Match 21.1%; Score 804; DB 6; Length 208;
Best Local Similarity 60.1%; Pred. No. 2.35e-137;
Matches 110; Conservative 36; Mismatches 36; Indels 1; Gaps 1;

Db 24 PGPLGDFKDDTSDRLTSPDKTEALIKYILGKISAMRKCEKYDKCNSKEALAEN 83
QY 342 PVPPGDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKETCNKSNMCESSKEALAEN 401
Db 84 NLNPKMAEKDGCFCGSGFNOETCLMRITTCGLLEYQIYLDYQNEYEGDKGIEAVQISSK 143
QY 402 NLNPKMAEKDGCFCGSGFNEETCLVKITGLLEFEVYLEYLNRFESSEEQARAVQMSTK 461
Db 144 ALAQILRQKVKNPDEVTTDPPTTNASIMNMQSONDDMKNTKIILRLSLENFLQFSLR 203
QY 462 VLIOFLQKRAKNLDAITDPPTTNASILLKLOAQNO-WLQDWTTHLLRSFKFLOSSLR 520
Db 204 AVR 206
QY 521 ALR 523

RESULT 6
ID O97535 PRELIMINARY; PRT; 160 AA.

AC O97535;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus vociferans.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
RN [1]
RP SEQUENCE FROM N.A.
RA ECHEVERRY S.J., HERNANDEZ E., MORENO A., PATARROYO M.E., MURILLO L.A.;
RT "Identification, cloning and sequencing of different interleukin genes
RT in 4 Aotus species."
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014505; AAD01531.1; -.
DR HSSP; P05231; 2IL6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1
SQ SEQUENCE 160 AA; 17855 MW; EF6090C3 CRC32;

Query Match 19.7%; Score 748; DB 6; Length 160;
Best Local Similarity 87.5%; Pred. No. 2.04e-125;
Matches 105; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Db 29 PVPLGDSKEVAAPNRQLTSTEQIDKHRYILEGIALRKEICDKSNMCESSKEALAEN 88
QY 342 PVPPGDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKETCNKSNMCESSKEALAEN 401
Db 89 NLNPKMAEKDGCFCGSGFNEETCLTKITGLLEFEVYLEYLNRFESSEEQAGAVQMSTK 148
QY 402 NLNPKMAEKDGCFCGSGFNEETCLVKITGLLEFEVYLEYLNRFESSEEQARAVQMSTK 461

RESULT 7
ID Q28403 PRELIMINARY; PRT; 207 AA.
AC Q28403;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Enhydra lutris (Sea otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Mustelidae; Enhydra.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96163018.
RA KING D.P., SCHRENZEL M.D., MCKNIGHT M.L., REIDARSON T.H., HANNI K.D.,
RA STOTT J.L., FERRICK D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:190-195(1996).
DR EMBL; I46804; AAB01428.1; -.
DR HSSP; P05231; 2IL6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR PFAM; PF00489; IL-6; 1.
FT NON_TER 1
SQ SEQUENCE 207 AA; 23527 MW; 0F2CAC62 CRC32;

Query Match 19.1%; Score 725; DB 6; Length 207;
Best Local Similarity 54.3%; Pred. No. 1.57e-120;
Matches 100; Conservative 42; Mismatches 40; Indels 2; Gaps 2;

Db 26 PGPLGDSKDDATSNRPPLTSADKMEFIKFIILGKISALRNEMCDKYNKCESKEVLAEN 85
QY 342 PVPPGDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKETCNKSNMCESSKEALAEN 401
Db 86 NLNPKLAEKDRCFCQSRFNOETCLTRITTTGLQEFQIHLKYLESNYEGKNDAHVIYSTK 145
QY 402 NLNPKMAEKDGCFCGSGFNEETCLVKITGLLEFEVYLEYLNRFESSEEQARAVQMSTK 461
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Db 146 HLIQTLRPM-NOIE-VTTPDPTDASIQALFKSQDKWLKHTTHILIRLREDFLQSLRA 203
QY 462 VLIQFLQKAKNLDATPTDPTTNASLLTKLQAOQWQLQDMTTHILIRSFKEFLQSSLR 521
Db 204 IRIM 207
QY 522 LRQ 525

RESULT 8
ID Q9WV08 PRELIMINARY; PRT; 210 AA.
AC Q9WV08;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DE 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE IL-6 (FRAGMENT).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-APA; TISSUE-KIDNEY;
RA NISHIDA E.;
RT "APA hamsters IL-6 partial cDNA.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB028635; BAA78766.1; -.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1
SQ SEQUENCE 210 AA; 24060 MW; 0307F113 CRC32;

Query Match 14.2%; Score 539; DB 11; Length 210;
Best Local Similarity 38.8%; Pred. No. 1.71e-81;
Matches 71; Conservative 51; Mismatches 59; Indels 2; Gaps 2;

Db 28 VRGDFTEQ-TTPNRPVYTSQVGLVTVYVIREIYELRKELCNPNPCMDNDYVLENN 86
QY 343 VPGEDSKDVAAPHROPLTSSRIDKQIRYILDGISAURKETCNKSNMCESSKEALANN 402
Db 87 LELPVIQDGLQGYNWEICLLKTSGLDYQIVLEFVTNNVDNKKDKARVIOSTIK 146
QY 403 LNLPKMAEKDGCFCGFSNETCLVKIITGLLEFVYLEYLQNR-ESSEQARAVQMSVK 461
Db 147 TISQIFKQVKGPKIVPSPRTSKAILMEKLESQKQEWPRTKIKILKALEEFLVTRMS 206
QY 462 VLIQFLQKAKNLDATPTDPTTNASLLTKLQAOQWQLQDMTTHILIRSFKEFLQSSLR 521
Db 207 TRQ 209
QY 522 LRQ 524

RESULT 9
ID Q88507 PRELIMINARY; PRT; 372 AA.
AC Q88507;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DE 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR.
GN CNTRF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN, SKELETAL MUSCLE;
RA MAEDA M., YAGUCHI N., HANYUU C., NAKATA Y., ONODA N., TULIN E.E.,
RA KOJIMA T., HASEGAWA M., KIKUCHI Y., NOMURA H.;
RT "Mouse homolog of human ciliary neurotrophic factor receptor.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF068615; AAC25711.1; -.
DR PFAM; PF00041; fn3; 1.
DR PFAM; PF00047; ig; 1.
KW Signal.

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FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 336 CILIARY NEUROTROPHIC FACTOR RECEPTOR
FT ALPHA.
SQ SEQUENCE 372 AA; 40831 MW; 9A40FE12 CRC32;

Query Match 10.9%; Score 413; DB 11; Length 372;
Best Local Similarity 32.7%; Pred. No. 9.20e-56;
Matches 102; Conservative 71; Mismatches 116; Indels 23; Gaps 20;

Db 11 AVLAAAAAAYTQKSPQAPHYQYERL-GADVTLP-C-GTASMD-AAVTW--RVNGTDLA 65
QY 11 ALLAAPGAALAPRCPAQEVARGVLTSLPGDSVLTLCGVEPEDNATVHWLKKPAAGSH 70
Db 66 PLLNG-SQ-LILRSLELHSGLYACFHRDSDWHLRHQVLLHVLGPPREPVLSC-RSNTYP 122
QY 71 PSRWAGMGRLLSRVQLHDSGNSCY-RAGRPAGTVHLL-VDPPEEPQLSCFRKSPLS 128
Db 123 KGFCYSW-HLPPTYIPNT-FNVTVLHGS---KIMV-CE-KDPALKNRCHIRYMHLSFI 175
QY 129 NVV-CWGPRTSPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFSQCLAVPEGDSF 187
Db 176 KYKVSISVSNALGHN-TTATITDEFITVPKPPENVAVRPVSPNRRLEVTWQTPSTWPD 234
QY 188 -YIVSMCVASSVSGSKFTQTQGGCGLQDPDPANITVTAVARNPWLSTVWQDPHSW-N 245
Db 235 PSFPLKFLRYRLPRLILDQWHLVSDGTAH-TTIDAYAGKEYIIQVAAKDN-EIGTWS 292
QY 246 SSFYRLRFELRYRAERSKFTTTVMVKDLQHHCVIHDWSGLRVVQLRAQEEFGQEWSE 305
Db 293 WSVAAAHATPWE 304
QY 306 WSPFAMGTPWE 317

RESULT 10
ID Q64385 PRELIMINARY; PRT; 432 AA.
AC Q64385;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NR1) (ETL2)
DE (IL-11RALPHA) (IL11RAL).
GN IL11RAL OR IL11RA OR ETL2 OR ETL2/IL11 REC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=LIVER;
RX MEDLINE; 95045367.
RA HILTON D.J., HILTON A.A., RAICEVIC A., RAKAR S., HARRISON-SMITH M.,
RA COUGH N.M., BEGLEY C.G., METCALF D., NICOLA N.A., WILLSON T.A.;
RT "Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130
RL for high affinity binding and signal transduction.";
RN EMO J. 13:4765-4775(1994).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C, AND C57BL/6; TISSUE=EMBRYO;
RA NEUHAUS H., BETTENHAUSEN B., BILINSKI P., SIMON-CHAZOTTES D.,
RA GUENET J.L., GOSSLER A.;
RL Dev. Biol. 166:521-542(1994).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C, AND C57BL/6;
RA GOSSLER A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97129000.
RA BILINSKI P., HALL M.A., NEUHAUS H., GISSEL C., HEATH J.K., GOSSLER A.;
RT "Two differentially expressed interleukin-11 receptor genes in the
RL mouse genome.";
RL Biochem. J. 320:359-363(1996).

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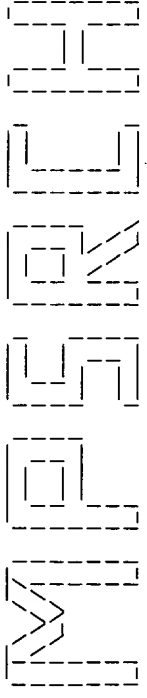

RP	SEQUENCE FROM N.A.	
RC	STRAIN-CD1; TISSUE-TESTIS;	
RX	MEDLINE; 97129000.	
RA	BILINSKI P., HALL M.A., NEUHAUS H., GISSEL C., HEATH J.K., GOSSLER A.	
RT	"Two differentially expressed interleukin-11 receptor genes in the	
RT	mouse genome.";	
RL	Biochem. J. 320:359-363(1996).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-CD-1; TISSUE-TESTIS;	
RX	STRAIN-CD-1; TISSUE-TESTIS;	
RX	MEDLINE; 96278810.	
RA	ROBB L., HILTON D.J., WILLSON T.A., BEGLEY C.G.;	
RT	"Structural analysis of the gene encoding the murine interleukin-11	
RT	receptor alpha-chain and a related locus.";	
RL	J. Biol. Chem. 271:13754-13761(1996).	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-CD-1; TISSUE-TESTIS;	
RX	MEDLINE; 97230451.	
RA	ROBB L., HILTON D.J., BROOK-CARTER P.T., BEGLEY C.G.;	
RT	"Identification of a second murine interleukin-11 receptor alpha-chain	
RT	gene (Il11ra2) with a restricted pattern of expression.";	
RL	Genomics 40:387-394(1997).	
CC	-1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.	
CC	-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.	
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	
CC	-1- TISSUE SPECIFICITY: WIDELY EXPRESSED.	
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS	
CC	ONE IG-LIKE DOMAIN.	
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.	
DR	EMBL; X94157; CAA63872.1; -	
DR	EMBL; X94158; CAA63872.1; JOINED.	
DR	EMBL; X94159; CAA63872.1; JOINED.	
DR	EMBL; X94160; CAA63872.1; JOINED.	
DR	EMBL; X94161; CAA63872.1; JOINED.	
DR	EMBL; X98519; CAA67144.1; -	
DR	EMBL; U69491; AAC53114.1; -	
DR	HSP; P16471; 1BP3.	
DR	MGD; MGI:109123; Il11ra2.	
DR	PFAM; PF00041; fn3; 2.	
DR	PFAM; PF00047; ig; 1.	
KW	Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.	
FT	SIGNAL	1 23
FT	CHAIN	24 432
FT	DOMAIN	24 367
FT	TRANS	368 393
FT	DOMAIN	394 432
FT	DOMAIN	41 102
FT	CARBOHYD	127 127
FT	CARBOHYD	194 194
FT	CONFLICT	200 200
FT	CONFLICT	384 384
FT	CONFLICT	432 AA; 46721 MW; C4FD7DEC CRC32;
SO	SEQUENCE	
	Query Match	10.5%; Score 400; DB 11; Length 432;
	Best Local Similarity	30.5%; Pred. No. 3.71e-53;
	Matches	99; Conservative 74; Mismatches 134; Indels 18; Gaps 1
Db	1	MSSSCSLTRVLVAVATALVSSSSPCQAWPGPVQYQGPGRVPMCLCPGV-SAG-TPVS 58
QY	2	LAVGCLALLAALLAAGCAALAPRCAP-AQE-VARGVLTSLPGDSVTLTCPGPEPDNATVP 59
Db	59	W-FRDGSRLLQCPDGGGLGRLVLAQVDSFDGTVYQCTLDGVSQGMVTLKLGPPPARPE 117
QY	60	WVLRKPAAGSHPSRWAGMRLLRSVQLHDSGNTSCYR-AGRPAQTWHLLVDVPPPEPQ 118
Db	118	VSC-QAVDYENFSCSPGVQSGVSLTPRYLTYSYRK-KTLPGAESQRESPESTGFWPCQDPL 175
QY	119	LSCFRKSPLSNVVCEVGPSTPSTLTAKVLLYRKQNSPAEDFQ-EPQCYSQ-E-SQK-F 174
Db	176	EASRCVVHGAFFNSFSEYRINVTENSLGASTCLLDVRLQ-SILRPPDPGLRVESVPGVPR 234
QY	175	-SCOLAVPEGD-SSFYIVNSCVASSVGSFKSTQTFQCGCLQPPDPAITVAVRNPR 232

Qy	2	LAVGCALLAALLAAPGAALAPRCP-AQE-VARGVLTSLPGDSVLTCPGSEPEDNATVH	59
Db	59	W-FRDGSRLLQPGDGLGRLVLAQVDSPDGTVYCOTLDGVSAGMKVTLKLGPPARPE	117
Qy	60	WYLKPKAAGSHPRWAGMGRLLRLRSVQLHDSGNTSCYR-AGRPAGTVHLLVDVPPPEPQ	118
Db	118	VSC-QAVDYENFNSCTSPGQVSGVLPYRLTYSRK-KTLPGAESQRESPTGWPWCQDPL	175
Qy	119	LSCFRKSPLSNVVCEWGRSTPSTLTAKVLLYRKQNSPAEDFQ-EPQCYSQ-E-SQK-F	174
Db	176	EASRCVVHGAEFNSFSEYRINVTENSLGASTCLLDVRLQ-SILRPPDPGLRVESVPGYPR	234
Qy	175	-SCOLAVPEGD-SSFTIVNSCVASSVGSFKSTQTFQCGILQPPPINATVAVNPR	232

DF 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.
RN [1]
RP SEQUENCE FROM N.A.
RA HEINE H., DELUDE R.D., MONKS B., GOLENECK D.T.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF044667; AAC02100.1; -
DR HSSP; P05231; 21L6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR PFAM; PF00489; IL-6; 1.
FT NON_TER 1
FT NON_TER 101
SQ SEQUENCE 101 AA; 11749 MW; D1DA362A CRC32;
Query Match 8.7%; Score 329; DB 11; Length 101;
Best Local Similarity 41.2%; Pred. No. 3.77e-39;
Matches 40; Conservative 28; Mismatches 28; Indels 1; Gaps 1;
Db 5 NDGCYQGYGYNWEICLLKITSGLLDYQIYLEFVTNNVQDNKKDKARVIOSTTKTLSQIFKQ 64
QY 411 KDGCFQSGFNEETCLVRIITGLLEFEVYLEVQLNRF-ESSEEQARAVQMSTKVLIQFLQK 469
Db 65 EVKDPDKIVMPSPISKALIEKLESQKQWPRTKTIEL 101
QY 470 KAKNLDAITTPDPTTNASLTLKLAQANQLQDMTHL 506

Search completed: Thu Aug 10 16:05:57 2000
Job time : 154 secs.

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(TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Aug 10 16:01:55 2000; MasPar time 17.41 Seconds
Tabular output not generated. 934.508 Million cell updates/sec

Title: >US-09-142-471-2
Description: (1-525) from US09142471.pep
Perfect Score: 3803
Sequence: 1 MLAVGCALLAALLAAPGAAL.....LILRSKFELQSSLRALRQW 525

Scoring table: PAM 150
Gap 11

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot38
1:swissprot

Statistics: Mean 50.832; Variance 91.281; scale 0.557

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2398	63.1	468	1	IL6A_HUMAN	0.00e+00
2	1356	35.7	462	1	IL6A_RAT	1.31e-273
3	1320	34.7	460	1	IL6A_MOUSE	3.19e-265
4	1287	33.8	212	1	IL6_HUMAN	1.53e-257
5	1257	33.1	212	1	IL6_MACFA	1.45e-250
6	1251	32.9	212	1	IL6_MACMU	3.59e-249
7	1244	32.7	212	1	IL6_CERTO	1.52e-247
8	814	21.4	209	1	IL6_PROVI	1.43e-148
9	810	21.3	205	1	IL6_ORCOR	1.16e-147
10	806	21.2	208	1	IL6_HORSE	9.40e-147
11	801	21.1	212	1	IL6_PIG	1.28e-145
12	786	20.7	207	1	IL6_CANFA	3.26e-142
13	786	20.7	208	1	IL6_FELCA	3.26e-142
14	693	18.2	208	1	IL6_BOVIN	3.27e-121
15	683	18.0	208	1	IL6_CAPHI	5.77e-119
16	680	17.9	208	1	IL6_SHEEP	2.72e-118
17	654	17.2	207	1	IL6_MARMO	1.83e-112
18	560	14.7	211	1	IL6_MOUSE	1.45e-91
19	558	14.7	211	1	IL6_RAT	4.00e-91
20	491	12.9	125	1	IL6_MUSVI	1.97e-76
21	407	10.7	372	1	CNTR_RAT	2.48e-58
22	403	10.6	372	1	CNTR_HUMAN	1.76e-57
23	373	9.8	362	1	CILIARY NEUTROPHIC F	3.88e-51


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QY 180 VPEGSSFFIVSMCVASSVGSFSTQTQFGCGILQDPPANITVTAVARNRWLSVTWQ 239
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
D 237 DPESMDPSYLLQFELRPVMSKFTVWPLQVAOHCQVHDALRGVKKVGVVGRKEEDF 296
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 240 DPHSNSSFYRLRFELRYRAERSKFTTWMVKDLQHCQVHDALRGVKKVGVVGRKEEDF 299
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
D 297 IGOWSKWSEVGTGTPWLAEPRTTPA 321
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 300 QGEWSEWSEPMGTW-TESRPPA 323
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

RESULT 3
ID IL6A_MOUSE STANDARD; PRT; 460 AA.
AC P22272;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1999 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA).
GN IL6RA OR IL6R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=SPLEEN;
RX MEDLINE; 90278354.
RA Sugita T., Totuska T., Saito M., Yamasaki K., Taga T., Hirano T.,
RA Kishimoto T.;
RT "Functional murine Interleukin 6 receptor with the intracisternal A
RT particle gene product at its cytoplasmic domain. Its possible role in
RT plasmacytomagenesis."
RT J. Exp. Med. 171:2001-2009(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-C3H; TISSUE=LIVER;
RA Florillo M.T., Ciliberto G., Dente L.;
RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
DR EMBL; X51975; CAA36237.1; -
DR EMBL; X53802; CAA37810.1; -
DR PIR; JLO145; JLO145.
DR PIR; S14543; S14543.
DR HSP; P16471; IBP3.
DR MGI; MGI:105304; IL6RA.
DR PFAM; PF00041; fn3; 1.
DR PFAM; PF00047; Ig; 1.
DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
KW SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 460
FT DOMAIN 21 357
FT TRANSMEM 358 385
FT DOMAIN 386 460
FT DOMAIN 40 99
FT DISULFID 47 92

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FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 162 173 BY SIMILARITY.
FT CARBOHYD 32 32 POTENTIAL.
FT CARBOHYD 55 55 POTENTIAL.
FT CARBOHYD 150 150 POTENTIAL.
FT CONFLICT 374 374 A -> R (IN REF. 2).
SQ SEQUENCE 460 AA; 50454 MW; F85C5906D08525C4 CRC64;

Query Match 34.7%; Score 1320; DB 1; Length 460;
Best Local Similarity 55.1%; Pred. No. 3.19e-265;
Matches 179; Conservative 58; Mismatches 82; Indels 6; Gaps 3;

D 1 MLTVGCTLLVALLAAPVALVLSGCRALRYANGTVTSPLCATVTLICPGKEAAGNVTIHW 60
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLSLPGDSVTLTCGVEPEDNATVHW 60
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
D 61 VY----SGSQNRWTTGNTLVLRVOLSDTGDLCSLNDHLVGTVPVPLVDVPPPEPKLS 116
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 61 VLKPKAAGSHPSRWAGMRLLRLSLVQLHDSGNSYCYRAGRPAAGTVHLLVDVPPPEPQLS 120
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
D 117 CPERKPLVNAICEWRPSSPTTKAVLFAKKTNTNGKSDFOVPCQYSQOLKSFSCQVE 176
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 121 CPERKPLSNVVCWGPSTPTTKAVLLVRKFQNSPAE--DFQEPQCYSQESQKFSQCLA 179
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
D 177 ILEGDKVYHIVSLCVANSVSGSSKSHNEAFHSLKAVQDPDPANLWVAIPGRPRWLKVSQ 236
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 180 VPEGSSFFIVSMCVASSVGSFSTQTQFGCGILQDPPANITVTAVARNRWLSVTWQ 239
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
D 237 HPETWDPYLLQFELRPVMSKFTVWPLQVAOHCQVHDALRGVKKVGVVGRKEED 296
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 240 DPHSNSSFYRLRFELRYRAERSKFTTWMVKDLQHCQVHDALRGVKKVGVVGRKEED 299
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
D 297 LGOWSEWSEVGTGTPWLAEPRTTPA 321
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 300 QGEWSEWSEPMGTW-TESRPPA 323
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

RESULT 4
ID IL6_HUMAN STANDARD; PRT; 212 AA.
AC P05231;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2)
DE (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR).
GN IL6 OR IFNB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE; 87065033.
RA Hirano T., Yasukawa K., Harada H., Taga T., Watanabe Y., Matsuda T.,
RA Kashiwamura S.-I., Nakajima K., Koyama K., Iwamatsu A., Tsunasawa S.,
RA Sakiyama F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.;
RT "Complementary DNA for a novel human interleukin (BSF-2) that induces
RT B lymphocytes to produce immunoglobulin."
RT Nature 324:73-76(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88082664.
RA Yasukawa K., Hirano T., Watanabe Y., Muratani K., Matsuda T.,
RA Nakai S., Kishimoto T.;
RT "Structure and expression of human B cell stimulatory factor-2
RT (BSF-2/IL-6) gene."
RL EMBO J. 6:2939-2945(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87067433.
RA May L.T., Helfgott D.C., Sehgal P.B.;
RT "Anti-beta-2-interferon antibodies inhibit the increased expression of
RT HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts:
RT structural studies of the beta 2 interferon involved."

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Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).
[4] SEQUENCE FROM N.A.
RN MEDLINE; 87053818.
RX Zilberstein A., Ruggieri R., Korn J.H., Revel M.;
RA "Structure and expression of cDNA and genes for human
RT interferon-beta-2, a distinct species inducible by growth-stimulatory
RT cytokines.";
RL EMBO J. 5:2529-2537(1986).
RN [5]
RN SEQUENCE FROM N.A.
RX MEDLINE; 89391958.
RA Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
RA Aarden L.A.;
RT "Molecular cloning and expression of hybridoma growth factor in
RT Escherichia coli.";
RL J. Immunol. 139:4116-4121(1987).
RN [6]
RN SEQUENCE FROM N.A.
RX MEDLINE; 89391958.
RA Tonouchi N., Miwa K., Karasuyama H., Matsui H.;
RA "Deletion of 3' untranslated region of human BSF-2 mRNA causes
RT stabilization of the mRNA and high-level expression in mouse NIH3T3
RT cells.";
RL Biochem. Biophys. Res. Commun. 163:1056-1062(1989).
RN [7]
RN SEQUENCE FROM N.A.
RX MEDLINE; 89193317.
RA Wong G., Wittek-Giannotti J., Hewick R., Clark S., Ogawa M.;
RA "Interleukin 6: identification as a hematopoietic colony-stimulating
RT factor.";
RL Behring Inst. Mitt. 83:40-47(1988).
RN [9]
RN SEQUENCE FROM N.A.
RX MEDLINE; 93178270.
RA Chen Q.Y.;
RT "Stable and efficient expression of human interleukin-6 cDNA in
RT mammalian cells after gene transfer.";
RL Chung-Hua Chung Liu Tsa Chih 14:340-344(1992).
RN [10]
RN SEQUENCE OF 30-63.
RX MEDLINE; 88154445.
RA van Damme J., van Beeumen J., Decock B., van Snick J., de Ley M.,
RA Billiau A.;
RT "Separation and comparison of two monokines with
RT lymphocyte-activating factor activity: IL-1 beta and hybridoma growth
RT factor (HGF). Identification of leukocyte-derived HGF as IL-6.";
RL J. Immunol. 140:1534-1541(1988).
RN [11]
RN SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING 1ST DISULFIDE BOND.
RX MEDLINE; 95154344.
RA Breton J., la Fiura A., Bertolero F., Orsini G., Valsasina B.,
RA Zillicotto R., de Filippis V., Polverino de Laureto P., Fontana A.;
RT "Structure, stability and biological properties of a N-terminally
RT truncated form of recombinant human interleukin-6 containing a single
RT disulfide bond.";
RL Eur. J. Biochem. 227:573-581(1995).
RN [12]
RN DISULFIDE BONDS.
RX MEDLINE; 89286115.
RA Clogston C.L., Boone T.C., Crandall B.C., Mendiaz E.A., Lu H.S.;
RT "Disulfide structures of human interleukin-6 are similar to those of
RT human granulocyte colony stimulating factor.";
RL Arch. Biochem. Biophys. 272:144-151(1989).
RN [13]
RN MUTAGENESIS.
RX MEDLINE; 91243808.
RA Luetticken C., Kruettgen A., Moeller C., Heinrich P.C., Rose-John S.;
RT "Evidence for the importance of a positive charge and an
RT alpha-helical structure of the C-terminus for biological activity of
RT human IL-6.";
RL FEBS Lett. 282:265-267(1991).
RN [14]
RN STRUCTURE BY NMR.
RX MEDLINE; 96134845.
RA Nishimura C., Watanabe A., Gouda H., Shimada I., Arata Y.;
RT "Folding topologies of human interleukin-6 and its mutants as studied
RT by NMR spectroscopy.";
RL Biochemistry 35:273-281(1996).
RN [15]
RN STRUCTURE BY NMR.
RX MEDLINE; 97303053.
RA Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
RA Cumming D.A.;
RT "Solution structure of recombinant human interleukin-6.";
RL J. Mol. Biol. 268:468-481(1997).
RN [16]
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE; 97224126.
RA Somers W., Stahl M., Seehra J.S.;
RT "1.9-A crystal structure of interleukin 6: implications for a novel
RT mode of receptor dimerization and signaling.";
RL EMBO J. 16:989-997(1997).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC
CC EMBL; X04430; CAA28026.1; -
CC EMBL; M14584; AAA52728.1; -
CC EMBL; X04602; CAA28268.1; -
CC EMBL; Y00081; CAA68278.1; -
CC EMBL; M18403; AAA52729.1; -
CC EMBL; M29150; AAA59154.1; -
CC EMBL; X04402; CAA27990.1; -
CC EMBL; X04403; CAA27991.1; -
CC EMBL; M54894; AAC41704.1; -
CC EMBL; S56892; AAD13886.1; -
CC EMBL; A09363; CAA00839.1; -
CC PIR; A32648; IVHUB2.
CC PIR; A25921; A25921.
CC PDB; 1IL6; 04-FEB-98.
CC PDB; 2IL6; 04-FEB-98.
CC PDB; 1ALU; 03-JUN-98.
CC MIN; 147620; -
CC PFAM; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC PRINTS; PR00434; INTERLEUKIN6.
CC PROSITE; PS00254; INTERLEUKIN6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal; 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78
FT DISULFID 101 111
FT CARBOHYD 73 73
FT MUTAGEN 173 173
FT MUTAGEN 185 185
FT A->V: ALMOST NO LOSS OF ACTIVITY.
FT W->R: NO LOSS OF ACTIVITY.

FT MUTAGEN 204 204 S->P: 13% ACTIVITY.
 FT MUTAGEN 210 210 R->K,E,Q,T,A,P: LOSS OF ACTIVITY.
 FT MUTAGEN 212 212 M->T,N,S,R: LOSS OF ACTIVITY.
 SQ SEQUENCE 212 AA; 23718 MW; 1F1ED1FE1B734079 CRC64;

Query Match 33.8%; Score 1287; DB 1; Length 212;
 Best Local Similarity 100.0%; Pred. No. 1.53e-257;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 29 PVPGGEDSKDVAAPHROPLTSSRIDKQIRYILDGTSALKRKTCKNSNMCSSEKEALAEN 88
 QY 342 PVPGGEDSKDVAAPHROPLTSSRIDKQIRYILDGTSALKRKTCKNSNMCSSEKEALAEN 401
 Db 89 NLNLPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLEYQNRFFSESEQARAVQMSK 148
 QY 402 NLNLPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLEYQNRFFSESEQARAVQMSK 461
 Db 149 VLIQFLQKRAKNLDAITTPDPTTNASLLTKLQAOQWLODMTHLILRSKFELQSSLA 208
 QY 462 VLIQFLQKRAKNLDAITTPDPTTNASLLTKLQAOQWLODMTHLILRSKFELQSSLA 521
 Db 209 LROM 212
 QY 522 LROM 525

RESULT 5
 ID IL6_MAFCA STANDARD; PRT; 212 AA.
 AC P79341.
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tatsumi M.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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 CC
 CC EMBL: AB000554; BAA19148.1; -
 CC HSSP: P05231; 21L6.
 CC PFAM: PF00489; IL6; 1.
 CC PRINTS: PR00433; IL6GCSFMGF.
 CC PROSITE: PS00254; INTERLEUKIN_6; 1.
 CC CYTOKINE; Glycoprotein; Growth factor; Signal.
 CC SIGNAL 1 29 BY SIMILARITY.
 CC CHAIN 30 212 INTERLEUKIN-6.
 CC DISULFID 72 78 POTENTIAL.
 CC FT DISULFID 101 111 POTENTIAL.
 CC FT CARBOHYD 73 73 POTENTIAL.
 CC FT CARBOHYD 172 172 POTENTIAL.
 CC SQ SEQUENCE 212 AA; 23654 MW; CF8173FCBF0B0389 CRC64;

Query Match 33.1%; Score 1257; DB 1; Length 212;

Best Local Similarity 96.7%; Pred. No. 1.45e-250;
 Matches 178; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 29 PVPGGEDSKDVAAPHROPLTSSRIDKQIRYILDGTSALKRKTCKNSNMCSSEKEALAEN 88
 QY 342 PVPGGEDSKDVAAPHROPLTSSRIDKQIRYILDGTSALKRKTCKNSNMCSSEKEALAEN 401
 Db 89 NLNLPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLEYQNRFFSESEQARAVQMSK 148
 QY 402 NLNLPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLEYQNRFFSESEQARAVQMSK 461
 Db 149 VLIQFLQKRAKNLDAITTPDPTTNASLLTKLQAOQWLODMTHLILRSKFELQSSLA 208
 QY 462 VLIQFLQKRAKNLDAITTPDPTTNASLLTKLQAOQWLODMTHLILRSKFELQSSLA 521
 Db 209 LROM 212
 QY 522 LROM 525

RESULT 6
 ID IL6_MACMU STANDARD; PRT; 212 AA.
 AC P51494;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RAC 2;
 RX MEDLINE; 96003435.
 RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and
 RT nonhuman primates";
 RL J. Immunol. 155:3946-3954(1995).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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 CC
 CC EMBL: L26028; AAA99978.1; -
 CC HSSP: P05231; 1AUU.
 CC PFAM: PF00489; IL6; 1.
 CC PRINTS: PR00433; IL6GCSFMGF.
 CC PROSITE: PS00254; INTERLEUKIN_6; 1.
 CC CYTOKINE; Glycoprotein; Growth factor; Signal.
 CC SIGNAL 1 29 BY SIMILARITY.
 CC CHAIN 30 212 INTERLEUKIN-6.
 CC DISULFID 72 78 POTENTIAL.
 CC FT DISULFID 101 111 POTENTIAL.
 CC FT CARBOHYD 73 73 POTENTIAL.
 CC FT CARBOHYD 172 172 POTENTIAL.
 CC SQ SEQUENCE 212 AA; 23728 MW; 4130DFE0CF0BCCAD CRC64;

Query Match 32.9%; Score 1251; DB 1; Length 212;
 Best Local Similarity 95.7%; Pred. No. 3.59e-249;
 Matches 176; Conservative 6; Mismatches 2; Indels 0; Gaps 0;


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QY 402 NUNLPMKAEKDCFCGSGFNEETCLVKIITGLLEFEVLEYLQNRFSSESEQARAVQMSTK 461
DB 146 LLVQMLKKVKVKSODEVTTDPDPTTDSLOAILKAQDKWLKHTTHILLRSLDFLOFSLRA 205
QY 462 VLIQFLOKKAKNLDAITTPDPTTNASLLTKLOAQONQWLQDMTHILLRSFKFLOSSLR 521
DB 206 VRIM 209
QY 522 LRQM 525

RESULT 9
ID IL6_ORCOR STANDARD; PRT; 205 AA.
AC Q28747;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DE 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
GN IL6.
OS Orcinus orca (Killer whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Orcinus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96163018.
RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
RA Stott J.L., Ferrick D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:190-195(1996).
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
DR EMBL; L46803; AAB01429.1; -.
DR HSP; P05231; IALU.
DR PFAM; PF00489; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT NON_TER 1 1
FT SIGNAL <1 21 BY SIMILARITY.
FT CHAIN 22 205 INTERLEUKIN-6.
FT DISULFD 64 70 BY SIMILARITY.
FT DISULFD 93 103 BY SIMILARITY.
FT CARBOHYD 164 164 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 205 AA; 23266 MW; 6308F3A457960832 CRC64;

Query Match 21.3%; Score 810; DB 1; Length 205;
Best Local Similarity 60.7%; Pred. No. 1.16e-147;
Matches 111; Conservative 36; Mismatches 35; Indels 1; Gaps 1;

DB 21 PGLPEDFKDDTTSRLYLTSPDKTEKILTKYILGISAMRKEMCKYDKCNSKEALAE 80
QY 342 PVPFGEDSKVAAPHRQPLTSSRTDKQIRYILDIGISALRKETCKNSKNCSSKEALAE 401
DB 81 NUNLPMKAEKDCFCGSGFNEETCLMRITTTGLLEYIYLDYQNEYGDKATEAVQISK 140
QY 402 NUNLPMKAEKDCFCGSGFNEETCLVKIITGLLEFEVLEYLQNRFSSESEQARAVQMSTK 461

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DB 141 ALAQILRQKVKNPDEVTTDPDPTTNASIMNLOSQNDMMKNTKIILIRSLNFLOFSLR 200
QY 462 VLIQFLOKKAKNLDAITTPDPTTNASLLTKLOAQONQWLQDMTHILLRSFKFLOSSLR 520
DB 201 AIR 203
QY 521 ALR 523

RESULT 10
ID IL6_HORSE STANDARD; PRT; 208 AA.
AC Q95181; O19007; O46568;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
RN [1]
RP SEQUENCE FROM N.A.
RA Swiderski C.E., Horohov D.W.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Leutenegger C.M., Huder J.B., von Rechenberg B., Akens M., Auer J.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Lai A.C.K.;
RT "Cloning and expression of equine interleukin-6.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
DR EMBL; U64794; AAB87703.1; -.
DR EMBL; AF005227; AAB62246.1; -.
DR EMBL; AF041975; AAC04574.1; -.
DR HSP; P05231; IALU.
DR PFAM; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSPMGF.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 208 INTERLEUKIN-6.
FT DISULFD 69 75 BY SIMILARITY.
FT DISULFD 98 108 BY SIMILARITY.
FT CARBOHYD 71 71 POTENTIAL.
FT CARBOHYD 184 184 POTENTIAL.
FT CONFLICT 4 5 LS -> FF (IN REF. 1).
FT CONFLICT 8 8 T -> A (IN REF. 3).
FT CONFLICT 137 137 I -> V (IN REF. 2).
FT CONFLICT 205 205 V -> I (IN REF. 3).
SQ SEQUENCE 208 AA; 23325 MW; A62F4C234056BF66 CRC64;

Query Match 21.2%; Score 806; DB 1; Length 208;
Best Local Similarity 59.2%; Pred. No. 9.40e-147;
Matches 109; Conservative 42; Mismatches 29; Indels 4; Gaps 3;

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Db 29 PLPLGED--E-TTNGPLLTADTKTKOHIKIVILGKISALKNMCNPNFSCENSKVLAEN 85
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 342 PVPGECDKVAAPHRQPLTSERIDKQIRYILDGIALRKETCNKSNMCSSKEALAEN 401
 Db 86 NLNPKMAKDCQFSGFNOETCLMKITGSEFQIYLEYLONFKEKENIKMTQISTK 145
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 402 NLNPKMAKDCQFSGFNEETCLVKITGLLEFEVYLEYLONFKESEEQARAVQMSTK 461
 Db 146 VLVOILQMKKNPE-VITPDPPTAKSSLLAKLHSONEWLKNWTHLILRSLEDFLOFSIRA 204
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 462 VLIQFLOKAKNLDATITPDTTNASLLTKLQAQNWQLQDMTHLILRSKFEFLQSSIRA 521
 Db 205 VRIM 208
 : | |
 QY 522 LRQM 525

RESULT 11
 ID IL6_PTG STANDARD; PRT; 212 AA.
 AC P26893;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91338547.
 RA Richards C., Saklatvala J.;
 RT "Molecular cloning and sequence of porcine interleukin 6 cDNA and
 RT expression of mRNA in synovial fibroblasts in vitro.";
 RL Cytokine 3:269-276(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92360284.
 RA Mathialagan N., Bibby J.A., Roberts M.R.;
 RT "Expression of interleukin-6 in porcine, ovine, and bovine
 RT preimplantation conceptuses.";
 RL Mol. Reprod. Dev. 32:324-330(1992).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M86722; AAC37333.1; -;
 CC EMBL; M80258; AAC27127.1; -;
 CC HSP; P05231; IALU.
 CC PFAM; PF00489; IL6; 1.
 CC PRINTS; PR00433; IL6GCSFMGF.
 CC PRINTS; PR00434; INTERLEUKIN6.
 CC PROSITE; PS00254; INTERLEUKIN.6; 1.
 CC Cytokine; Glycoprotein; Growth factor; Signal.
 CC SIGNAL 1 29 BY SIMILARITY.
 CC CHAIN 30 212 INTERLEUKIN-6.
 CC DISULFID 72 78 BY SIMILARITY.
 CC FT DISULFID 101 111 BY SIMILARITY.
 CC FT CONFLICT 30 30 G -> E (IN REF. 2).
 CC SEQUENCE 212 AA; 23880 MW; EF100ED030B6FDD0 CRC64;

Query Match 21.1%; Score 801; DB 1; Length 212;
 Best Local Similarity 59.8%; Pred. No. 1.28e-145;
 Matches 107; Conservative 37; Mismatches 35; Indels 0; Gaps 0;
 Db 34 EDKAGDATSKMLFTSPDKTEELIKYILGKISAMRCKMCKEYKENSKEVLAENNLNP 93
 ||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 347 EDKDAAPHRQPLTSERIDKQIRYILDGIALRKETCNKSNMCSSKEALAENNLNP 406
 Db 94 KMAEKDCQFSGFNOETCLMRITGVEFQIYLDYLOKYESNKNVAVQISTKALIQT 153
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 407 KMAEKDCQFSGFNEETCLVKITGLLEFEVYLEYLONFKESEEQARAVQMSTKVLQF 466
 Db 154 LRQKGNPDKATPNTNAGLLDKLQSQNEMKNTKIIILSLSEDFLOFSLRPRIM 212
 : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 467 LQKAKNLDATITPDTTNASLLTKLQAQNWQLQDMTHLILRSKFEFLQSSLRALQM 525

RESULT 12
 ID IL6_CANFA STANDARD; PRT; 207 AA.
 AC P41323;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MONGREL;
 RX MEDLINE; 94303924.
 RA Kukielka G.L., Youker K.A., Hawkins H.K., Perrard J.L.,
 RA Michael L.H., Ballantyne C.M., Smith C.W., Entman M.L.;
 RT "Regulation of ICAM-1 and IL-6 in myocardial ischemia: effect of
 RT reperfusion";
 RL Ann. N.Y. Acad. Sci. 723:258-270(1994).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U12234; AAA83030.1; -;
 CC HSP; P05231; 2IL6.
 CC PFAM; PF00489; IL6; 1.
 CC PRINTS; PR00433; IL6GCSFMGF.
 CC PRINTS; PR00434; INTERLEUKIN6.
 CC PROSITE; PS00254; INTERLEUKIN.6; 1.
 CC Cytokine; Glycoprotein; Growth factor; Signal.
 CC SIGNAL 1 29 POTENTIAL.
 CC CHAIN 30 207 INTERLEUKIN-6.
 CC DISULFID 67 73 BY SIMILARITY.
 CC FT DISULFID 96 106 BY SIMILARITY.
 CC SEQUENCE 207 AA; 22945 MW; 45540154EA9C0F50 CRC64;

Query Match 20.7%; Score 786; DB 1; Length 207;
 Best Local Similarity 58.2%; Pred. No. 3.26e-142;
 Matches 107; Conservative 37; Mismatches 40; Indels 0; Gaps 0;
 Db 24 PGPLAGDSKDDATNSPLTSANKVEELIKYILGKISALRCKMCKDNKNCDSKEALAEN 83
 : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 342 PVPGECDKVAAPHRQPLTSERIDKQIRYILDGIALRKETCNKSNMCSSKEALAEN 401

Db 84 NLHLPKLEGRDGFQSGFNOETCLTRITTLGLVEFQLHLNLONNYEGDKENKSVHMSTK 143
 QY 402 NLNPKMAEKDGCQSGFNEETCLVKIITGLLEFVLEYNRFESSEQARAVQMSTK 461
 Db 144 ILVQMLKSKVKNQDEVTTPPTDASLQALQSQDECVKHTTHLILRSLEDFLQSLRA 203
 QY 462 VLQFOFLOKKAENLDAITPPTDPTNASLLTKLOQNOWLODMTHLILRSFKEFLQSLRA 521
 Db 204 VRIM 207
 QY 522 LRQM 525
 RESULT 13
 ID IL6_FELCA STANDARD; PRT; 208 AA.
 AC P41683;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94162386.
 RA Hasegawa A.; Matsumoto Y., Watari T., Goitsuka R., Tsujimoto H.,
 RT "Molecular cloning of feline interleukin-6 cDNA.";
 RL J. Vet. Med. Sci. 55:941-944(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LYMPHOCTES;
 RX MEDLINE; 94052249.
 RA Bradley W.G., Gibbs C., Kraus L., Good R.A., Day N.K.;
 RT "Molecular cloning and characterization of a cDNA encoding feline
 interleukin-6.";
 RL Proc. Soc. Exp. Biol. Med. 204:301-305(1993).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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 CC -----
 CC EMBL; L16914; AAAL6620.1; -
 DR EMBL; D13227; BAA02507.1; -
 DR HSSP; P05231; 2IL6.
 DR PFAM; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR CYTOKINE; Glycoprotein; Growth factor; Signal.
 KW SIGNAL 1 27
 FT CHAIN 28 208
 FT DISULFID 68 74
 FT DISULFID 97 107
 FT CONFLICT 2 2
 FT CONFLICT 45 45
 FT CONFLICT 133 133
 FT CONFLICT 173 187
 FT CONFLICT 200 201
 FT CONFLICT 208 AA; 23401 MW; 93B4456B2989CA4C CRC64;
 SQ SEQUENCE

Query Match 20.7%; Score 786; DB 1; Length 208;
 Best Local Similarity 57.8%; Pred. No. 3.26e-142;
 Matches 100; Conservative 40; Mismatches 33; Indels 0; Gaps 0;
 Db 36 ATSNRLPLTSADKMEELIKYILGKISALKKEMCDNYKNKEDSKALAEENLNLPKAEKD 95
 QY 353 AAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNWCESSKALAEENLNLPKAEKD 412
 Db 96 GCFOSGNETCLTRITTTGLQEFQIYKLFQDYEGDEENAKSVYTTNVLQMLKRGK 155
 QY 413 GCFOSGNETCLVKIITGLLEFVLEYNRFESSEQARAVQMSTKVLQFLOKKA 472
 Db 156 NODEVTIPVPTVEVGLQAKLQSQEELRHTTHLILRLERDFLOFSLRVRIM 208
 QY 473 NLDAITTPDPTNASLLTKLOQNOWLODMTHLILRSFKEFLQSLRALQRM 525
 RESULT 14
 ID IL6_BOVIN STANDARD; PRT; 208 AA.
 AC P26892;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HOLSTEIN;
 RX MEDLINE; 93076003.
 RA Droogmans L., Cluets I., Cleuter Y., Kettmann R., Burny A.;
 RT "Nucleotide sequence of bovine interleukin-6 cDNA.";
 RL DNA Seq. 2:411-413(1992).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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 CC -----
 CC EMBL; X57317; CAA40572.1; -
 DR EMBL; S22162; S22162.
 DR HSSP; P05231; 2IL6.
 DR PFAM; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR CYTOKINE; Glycoprotein; Growth factor; Signal.
 KW SIGNAL 1 29
 FT CHAIN 30 208
 FT DISULFID 72 78
 FT DISULFID 101 111
 FT CARBOHYD 38 38
 FT POTENTIAL.
 SQ SEQUENCE 208 AA; 23758 MW; AOF000B9BA2EC341 CRC64;
 Query Match 18.2%; Score 693; DB 1; Length 208;
 Best Local Similarity 51.1%; Pred. No. 3.27e-121;
 Matches 93; Conservative 46; Mismatches 39; Indels 4; Gaps 2;
 Db 29 PGLGSEDFKNDTTPGRLTLTPKTEALIKRMVDKISAMRKEICEKNDECESSKETLAEN 88

Qy 342 PVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISAIRKRETCNKNMCESSKEALAE 401
Db 89 KLNLPKMEKDCGFCQSGNQAICLIRTAGLEQIYLDYLONEYEGNOENVDRDKNIR 148
Qy 402 NLNLPKMAEKDCGFCQSGNETCLVKIITGLLEFEVYLEYLONRFPESSEQARAVQMSTK 461
Db 149 TLIQILKQKIADL--ITTP--ATNTDLERKMSSNEWKNAKIILIRNLNLEFLQFSIRA 204
Qy 462 VLIQFLQKKAKNLDATITPDPPTTNASLLTKLQAOQNQLQDMTTHILRSFKFLOSSLRA 521
Db 205 IR 206
Qy 522 LR 523

RESULT 15
ID IL6_CAPHI STANDARD; PRT; 208 AA.
AC Q28319;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Capra.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97392354.
RA Takakura H., Mori Y., Tatsumi M.;
RT "Molecular cloning of caprine IL-6 cDNA and its expression in insect
cells";
RL Int. Arch. Allergy Immunol. 113:409-416(1997).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
CC EMBL; D86569; BAA13118.1; -
CC HSSP; P05231; 2IL6.
CC PFAM; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC PRINTS; PR00434; INTERLEUKIN_6.
CC PROSITE; PS00254; INTERLEUKIN_6; 1.
CC Cytokine; Glycoprotein; Growth factor; Signal.
CC SIGNAL 1 29 BY SIMILARITY.
CC CHAIN 30 208 INTERLEUKIN-6.
CC DISULFID 72 78 BY SIMILARITY.
CC DISULFID 101 111 BY SIMILARITY.
CC CARBOHYD 38 38 POTENTIAL.
CC SEQUENCE 208 AA; 23423 MW; E92E08BF3E3230A0 CRC64;

Query Match 18.0%; Score 683; DB 1; Length 208;
Best Local Similarity 51.1%; Pred. No. 5.77e-119;
Matches 93; Conservative 43; Mismatches 42; Indels 4; Gaps 2;
Db 29 PGPAGEDFNDDTTSRLTLTPKTEALIKHVDKISAIRKEICEDNCKENSKETLAEN 88
Qy 342 PVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISAIRKRETCNKNMCESSKEALAE 401
Db 89 KLNLPKMEKDCGFCQSGNQAICLIRTAGLEQIYLDYLONEYEGNOENVDRDKNIR 148
:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 402 NLNLPKMAEKDCGFCQSGNETCLVKIITGLLEFEVYLEYLONRFPESSEQARAVQMSTK 461
Db 149 TLIQILKQKIADL--ITTP--ATNTDLERKMSSNEWKNAKIILIRNLNLEFLQFSIRA 204
Qy 462 VLIQFLQKKAKNLDATITPDPPTTNASLLTKLQAOQNQLQDMTTHILRSFKFLOSSLRA 521
Db 205 IR 206
Qy 522 LR 523
Search completed: Thu Aug 10 16:03:06 2000
Job time : 71 secs.

W A R E A (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Aug 10 16:00:16 2000; MasPar time 27.06 Seconds
Tabular output not generated. 915.129 Million cell updates/sec

Title: >US-09-142-471-2
Description: (1-525) from US09142471.pep
Perfect Score: 3803
Sequence: 1 MLAVGCALLAALLAAGPAAAL.....LILRSFKFELQSSLRALRQM 525

Scoring table: PAM 150
Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r64
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 50.071; Variance 102.843; scale 0.487

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2398	63.1	468	1 A41242	interleukin-6 recepto	0.00e+00
2	1320	34.7	440	2 JI0144	interleukin-6 recepto	5.97e-232
3	1320	34.7	460	2 JI0145	interleukin-6 recepto	5.97e-232
4	1287	33.8	212	1 IVH082	interleukin-6 precurs	3.14e-225
5	1090	28.7	462	1 A37986	interleukin-6 recepto	2.93e-185
6	806	21.2	208	2 T09216	interleukin-6 precurs	2.88e-128
7	801	21.1	212	2 I46590	interleukin 6 - pig	2.85e-127
8	801	21.1	212	2 I46621	prointerleukin 6 - pi	2.85e-127
9	693	18.2	208	1 A56610	interleukin-6 precurs	6.67e-106
10	680	17.9	207	2 I46084	interleukin 6 - cat	2.40e-103
11	679	17.9	208	1 S29549	interleukin-6 - sheep	3.78e-103
12	560	14.7	211	1 ICMS6	interleukin-6 precurs	6.17e-80
13	558	14.7	211	2 A34247	interleukin-6 precurs	1.50e-79
14	407	10.7	372	2 T58141	ciliary neurotrophic	8.25e-51
15	403	10.6	372	1 UHHUCN	ciliary neurotrophic	4.60e-50
16	401	10.5	432	2 I48343	interleukin-11 recept	1.08e-49
17	377	9.9	422	2 T37891	interleukin-11 recept	3.07e-45
18	373	9.8	362	2 S60614	growth promoting acti	1.68e-44
19	212	5.6	831	2 J01655	prolactin receptor pr	3.82e-16
20	179	4.7	201	2 A42247	myelomonocytic growth	7.32e-11
21	179	4.7	581	2 I45971	prolactin receptor -	7.32e-11
22	172	4.5	830	2 I50455	prolactin receptor -	8.83e-10
23	165	4.3	630	2 I51086	prolactin receptor -	1.03e-08

24	155	4.1	917	2 I49699	glycoprotein 130 - mo	3.18e-07
25	152	4.0	616	2 A30304	prolactin receptor 2	8.74e-07
26	144	3.8	622	2 A40144	prolactin receptor lo	1.24e-05
27	142	3.7	206	2 A57018	prolactin receptor -	2.39e-05
28	140	3.7	310	2 A29884	prolactin receptor pr	4.58e-05
29	140	3.7	412	2 A41070	prolactin receptor Nb	4.58e-05
30	140	3.7	610	2 A36116	prolactin receptor 2	4.58e-05
31	140	3.7	610	2 A34631	lactogen receptor 1 -	4.58e-05
32	141	3.7	918	2 A36337	membrane glycoprotein	3.31e-05
33	139	3.7	918	2 A44257	interleukin-6 signal	6.37e-05
34	138	3.6	265	2 S14081	erythropoietin recept	8.74e-05
35	137	3.6	292	2 I77525	prolactin receptor pr	1.20e-04
36	137	3.6	303	2 I77524	prolactin receptor pr	1.20e-04
37	137	3.6	608	2 I53269	prolactin receptor, 1	1.20e-04
38	129	3.4	805	2 JC4897	leptin receptor, Ob-R	1.49e-03
39	129	3.4	894	2 JC4797	leptin receptor precu	1.49e-03
40	129	3.4	895	2 S74225	leptin receptor, isof	1.49e-03
41	129	3.4	1162	2 PC4184	leptin receptor, Ob-R	1.49e-03
42	125	3.3	206	2 I53066	gene M-twist protein	5.10e-03
43	127	3.3	328	2 A38957	interleukin 12B precu	2.77e-03
44	124	3.3	894	2 S68437	leptin receptor (vari	6.91e-03
45	125	3.3	1084	2 T04103	sucrose-phosphate syn	5.10e-03

ALIGNMENTS

RESULT	1
ENTRY	A41242
TITLE	interleukin-6 receptor precursor - human
CONTAINS	interleukin-6 receptor, soluble form
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	27-Mar-1992 #sequence_revision 02-Dec-1994 #text_change 22-Jun-1999
ACCESSIONS	A41242; JU0080; S17468; A61459; S14621
REFERENCE	A41242
#authors	Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, T.; Hirano, T.; Kishimoto, T.
#journal	Science (1988) 241:825-828
#title	Cloning and expression of the human interleukin-6 (BSF-2/IFNbeta 2) receptor.
#cross-references	MUID:88305347
#accession	A41242
#molecule_type	mRNA
#residues	1-468 #label YAM
#cross-references	GB:M20566; NID:g186346; PID:g307062
REFERENCE	JU0080
#authors	Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, T.; Hirano, T.; Kishimoto, T.
#journal	Proc. Jpn. Acad. (1988) 64:209-211
#title	Molecular structure of interleukin 6 receptor.
#accession	JU0080
#molecule_type	mRNA
#residues	1-468 #label YA2
REFERENCE	S17468
#authors	Schoellink, H.; Stoyan, T.; Lenz, D.; Schmitz, H.; Hirano, T.; Kishimoto, T.; Heinrich, P.C.; Rose-John, S.
#journal	Biochem. J. (1991) 277:659-664
#title	Structural and functional studies on the human hepatic interleukin-6 receptor. Molecular cloning and overexpression in HepG2 cells.
#cross-references	MUID:91336983
#accession	S17468
#molecule_type	mRNA
#residues	1-468 #label SCH
#cross-references	EMBL:X58298; NID:g32580; PIDN:CAA41231.1; PID:g32581
#experimental_source	hepatoma cell line HepG2
REFERENCE	A61459
#authors	Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M.
#journal	J. Exp. Med. (1989) 170:1409-1414
#title	Soluble cytokine receptors are present in normal human urine.
#cross-references	MUID:90010793
#accession	A61459
#molecule_type	protein


```

##residues      20-49 ##label NOV
COMMENT      Through this receptor, interleukin-6 induces proliferation,
              activation, and differentiation of various cell types.
COMMENT      This growth factor receptor does not have a tyrosine kinase domain.
GENETICS
#gene      GDB:IL6R
##cross-references GDB:127966; OMIM:147880
#map_position lq21-lq21
CLASSIFICATION #superfamily ciliary neurotrophic factor receptor; cytokine
               receptor homology; immunoglobulin homology
KEYWORDS      acute phase; cytokine receptor; glycoprotein; transmembrane
               protein
FEATURE
1-19          #domain signal sequence #status predicted #label SIG\
20-468       #product interleukin-6 receptor #status predicted #label
               MAT\
20-363       #domain extracellular #status predicted #label EXT\
40-98        #domain immunoglobulin homology #label IMM2\
121-309      #domain cytokine receptor homology #label CRS\
364-386      #domain transmembrane #status predicted #label TMM\
387-468      #domain intracellular #status predicted #label INT\
47-96        #disulfide_bonds #status predicted\
55,93,221,245,350 #binding_site carbohydrate (Asn) (covalent) #status
               predicted
SUMMARY      #length 468 #molecular-weight 51547 #checksum 4661

Query Match      63.1%; Score 2398; DB 1; Length 468;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLAVGCCALLAALAAPCAALAPRCAPAEVARGVLTSLPGDSVTLTCTCPGVEPEDNATVHW 60
QY 1 MLAVGCCALLAALAAPCAALAPRCAPAEVARGVLTSLPGDSVTLTCTCPGVEPEDNATVHW 60

Db 61 VLKRPAGSHPSRWAGMGRLLRSVLQHDGNYSCYRAGRAGTGVHLLVDVPPPEPKLS 120
QY 61 VLKRPAGSHPSRWAGMGRLLRSVLQHDGNYSCYRAGRAGTGVHLLVDVPPPEPKLS 120

Db 121 CFRKSPLSNVVCEWGPSTPSLTAKVLLVRKFQNSPAEDFQPCQYSDSQSFSCQLAV 180
QY 121 CFRKSPLSNVVCEWGPSTPSLTAKVLLVRKFQNSPAEDFQPCQYSDSQSFSCQLAV 180

Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFCGCGILQDPPANITVTAVARNPRLVSTWQD 240
QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFCGCGILQDPPANITVTAVARNPRLVSTWQD 240

Db 241 PHSWNSFFYLRFLRYRAERSKFTFTWMVKDLOHCHVHDANSGLRHVVQLRAQEEFG 300
QY 241 PHSWNSFFYLRFLRYRAERSKFTFTWMVKDLOHCHVHDANSGLRHVVQLRAQEEFG 300

Db 301 GEWSEWSPAMGTPWTESRSPA 323
QY 301 GEWSEWSPAMGTPWTESRSPA 323

RESULT 2
ENTRY      JLO144 #type complete
TITLE      interleukin-6 receptor precursor (clone lambda p1) - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
ACCESSIONS JLO144
REFERENCE   JLO144
#authors   Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.;
#journal   Hirano, T.; Kishimoto, T.
#title     Functional murine interleukin 6 receptor with the
           intracisternal a particle gene product at its cytoplasmic
           domain: its possible role in plasmacytomagenesis.
#cross-references MUID:90278354
#accession JLO144
#molecule_type mRNA
#status     nucleic acid sequence not shown
##residues 1-373, 'R', 375-460 ##label FTO
##cross-references EMBL:X53802; NID:g52692; PIDN:CAA37810.1; PID:g52693
CLASSIFICATION #superfamily ciliary neurotrophic factor receptor; cytokine

```

```

##residues      1-440 ##label SUG
##cross-references GB:X51976; NID:g53548; PIDN:CAA36238.1; PID:g53549
CLASSIFICATION #superfamily ciliary neurotrophic factor receptor; cytokine
               receptor homology; immunoglobulin homology
KEYWORDS      cytokine receptor; transmembrane protein
FEATURE
1-19          #domain signal sequence #status predicted #label SIG\
20-440       #product interleukin-6 receptor #status predicted #label
               MAT\
117-306      #domain cytokine receptor homology #label CRS\
358-385      #domain transmembrane #status predicted #label TRA
SUMMARY      #length 440 #molecular-weight 47901 #checksum 5876

Query Match      34.7%; Score 1320; DB 2; Length 440;
Best Local Similarity 55.1%; Pred. No. 5.97e-232;
Matches 179; Conservative 58; Mismatches 82; Indels 6; Gaps 3;

Db 1 MLFVGGTLLVALLAAPVALVLSGCRALAEVANGTVTSLPGATVTLICPGKEAAGNVTIHW 60
QY 1 MLAVGCCALLAALAAPCAALAPRCAPAEVARGVLTSLPGDSVTLTCTCPGVEPEDNATVHW 60

Db 61 VY----SGSONRRTTGTNLTLDVQLSDTGDYLCSLNDHLVGTVPVLLVDVPPPEPKLS 116
QY 61 VLKRPAGSHPSRWAGMGRLLRSVLQHDGNYSCYRAGRAGTGVHLLVDVPPPEPKLS 120

Db 117 CFRKNPLVNAICEWRPSSTPSTTKAVLFAKINTNGKSDFOVPCQYSDQLKSFSCQVE 176
QY 121 CFRKSPLSNVVCEWGPSTPSLTAKVLLVRKFQNSPAEDFQPCQYSDSQSFSCQLA 179

Db 177 ILEGDKVYHIVLCVANSVSGSKSHNEAFHSLKMWOPDPANLVSAIPGRPRLWKVSWQ 236
QY 180 VPEGDSSFYIVSMCVASSVSGSKFTQTFCGCGILQDPPANITVTAVARNPRLVSTWQ 239

Db 237 HPETWDPYVLLQFOLRYRPVWSKEFTVLLPVAQYOCVLDHALRGVKHVQVGRKEELD 296
QY 240 DPHSWNSFFYLRFLRYRAERSKFTFTWMVKDLOHCHVHDANSGLRHVVQLRAQEEFG 299

Db 297 LGQWSEWSPAMGTPWTESRSPA 321
QY 300 GEWSEWSPAMGTPWTESRSPA 323

RESULT 3
ENTRY      JLO145 #type complete
TITLE      interleukin-6 receptor precursor (clone lambda 301) - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
ACCESSIONS JLO145; S14543
REFERENCE   JLO144
#authors   Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.;
#journal   Hirano, T.; Kishimoto, T.
#title     Functional murine interleukin 6 receptor with the
           intracisternal a particle gene product at its cytoplasmic
           domain: its possible role in plasmacytomagenesis.
#cross-references MUID:90278354
#accession JLO145
#molecule_type mRNA
#status     nucleic acid sequence not shown
##residues 1-460 ##label SUG
##cross-references GB:X51975; NID:g49725; PIDN:CAA36237.1; PID:g49726
REFERENCE   S14543
#authors   Fiorillo, M.T.; Ciliberto, G.; Dente, L.
#journal   submitted to the EMBL Data Library, July 1990
#title     Cloning and expression of murine IL-6 receptor.
#accession S14543
#status     preliminary
#molecule_type mRNA
#residues 1-373, 'R', 375-460 ##label FTO
##cross-references EMBL:X53802; NID:g52692; PIDN:CAA37810.1; PID:g52693
CLASSIFICATION #superfamily ciliary neurotrophic factor receptor; cytokine

```



```
receptor homology; immunoglobulin homology
cytokine receptor; transmembrane protein
1-19
#domain signal sequence #status #predicted #label SIG\
#product interleukin-6 receptor #status predicted #label
MAT\
117-306 #domain cytokine receptor homology #label CRS\
358-385 #domain transmembrane #status predicted #label TRA
SUMMARY #length 460 #molecular-weight 50454 #checksum 1296

Query Match 34.7%; Score 1320; DB 2; Length 460;
Best Local Similarity 55.1%; Pred. No. 5.97e-232;
Matches 179; Conservative 58; Mismatches 82; Indels 6; Gaps 3;

Db 1 MLTVGCTLLVALLAALVILGSCALVAVGTVTSLPGATVTLICPGKEAGNVTHW 60
QY 1 MLAVGCALLAALLAALGAAALPRCPAGEVARGVLTSLPGDSVILTCGVPEDNATVHW 60
Db 61 VY----SGSQNRWTTGNTLVLRDVLQSDGDLVCLSLNDHLVGTPLVLLVDVPPPEPKLS 116
QY 1 VLRKPAAGSHPSWAGMGRRLRLSVQLHDSGNYSCYRAGRAGTGVHLLVDVPPPEPKLS 120
Db 117 CFRKNPLVNAICEWRPSTPPTTKAVLFAKKINTNGKSDFOVPCQYSQOLKSFSCOVE 176
QY 121 CFRKSPLSNVCEWRPSTPPTTKAVLLVRKFNQSPAE-DFQEPQYQSQESKFSCOLA 179
Db 177 ILEGDKVYHIVSLCVANSVSGSKSHNEAFHSLKMWQDPPANLVVSAIPGRPLKYSWQ 236
QY 180 VPEDSSEFYIVSMCVANSVSGSKFKTQTFQCGILQPPDPANIVTAVARNRMLSVTWQ 239
Db 237 HPETWDSYLLQFOLRPVPMKFTVLLPVAQYQCQVIHDALRGKHVVQVVRGKEELD 296
QY 240 DPHSWNSFYRLRFELRYRAERSKFTTWMVKDLQHCVIHDWGLRHVVQLRAQBEFG 299
Db 297 LQGNSEWSPEVTGPTWAEPTTFA 321
QY 300 QGEWSEWSPEAMGTPW-TESRSPA 323

RESULT 4
ENTRY IVHUB2 #type complete
ALTERNATE_NAMES interleukin-6 precursor - human
TITLE B-cell differentiation factor; B-cell hybridoma growth
factor; B-cell stimulating factor 2 (BSF-2); CTL
differentiation factor; IL-6; interferon beta-II-a;
megakaryocyte potentiation factor
ORGANISM #formal_name Homo sapiens #common_name man
DATE 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change
22-Jun-1999
ACCESSIONS A32648; A25692; A26966; A33515; A25801; A25921; I52193;
I56003; A27601; B27601; A60400; A29085; A61159; A61462;
A48419; C48419; B48419; JX0305; S04982
REFERENCE A32648
#authors Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.;
Matsuda, T.; Nakai, S.; Kishimoto, T.
#journal EMBO J. (1987) 6:2939-2945
#title Structure and expression of human B cell stimulatory factor-2
(BSF-2/IL-6) gene.
#cross-references MUID:88082664
#accession A32648
#molecule_type DNA
#residues 1-212 #label VAS
#cross-references GB:Y00081; NID:929494; PIDN:CAA68278.1; PID:g29495
#note the authors translated the codon CAG for residue 130 as
Glu
A91051
REFERENCE
#authors Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.
#journal EMBO J. (1986) 5:2529-2537
#title Structure and expression of cDNA and genes for human
interferon-beta-2, a distinct species inducible by
growth-stimulatory cytokines.
#cross-references MUID:87053818
#accession A25692
```

```
#molecule_type mRNA
#residues 1-212 #label ZIL
#cross-references GB:X04430; NID:g32673; PIDN:CAA28026.1; PID:g32674
REFERENCE A93387
#authors Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.;
Matsuda, T.; Kashiwamura, S.I.; Nakajima, K.; Koyama, K.;
Iwamatsu, A.; Tsunasawa, S.; Sakiyama, F.; Matsui, H.;
Takahara, Y.; Taniguchi, T.; Kishimoto, T.
#journal Nature (1986) 324:73-76
#title Complementary DNA for a novel human interleukin (BSF-2) that
induces B lymphocytes to produce immunoglobulin.
#cross-references MUID:87065033
#accession A26966
#molecule_type mRNA
#residues 1-212 #label HUR
#cross-references GB:X04602; NID:g33849; PIDN:CAA28268.1; PID:g33850
REFERENCE A33515
#authors Tonouchi, N.; Miwa, K.; Karasuyama, H.; Matsui, H.
#journal Biochem. Biophys. Res. Commun. (1989) 163:1056-1062
#title Deletion of 3' untranslated region of human BSF-2 mRNA causes
stabilization of the mRNA and high-level expression in
mouse NIH3T3 cells.
#cross-references MUID:89391958
#accession A33515
#molecule_type mRNA
#residues 1-212 #label TON
#cross-references GB:M29150; NID:gl86349; PIDN:AAA59154.1; PID:g307063
REFERENCE A25801
#authors Haegeman, G.; Content, J.; Volckaert, G.; Derynck, R.;
Tavernier, J.; Fiers, W.
#journal Eur. J. Biochem. (1986) 159:625-632
#title Structural analysis of the sequence coding for an inducible
26-kDa protein in human fibroblasts.
#cross-references MUID:87004683
#accession A25801
#molecule_type DNA; mRNA
#residues 1-212 #label HAE
#cross-references GB:X04403
#experimental_source fibroblast
REFERENCE A25921
#authors May, L.T.; Helfgott, D.C.; Sehgal, P.B.
#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:8957-8961
#title Anti-beta-interferon antibodies inhibit the increased
expression of HUA-B7 mRNA in tumor necrosis factor-treated
human fibroblasts: structural studies of the beta-2
interferon involved.
#cross-references MUID:87067433
#accession A25921
#molecule_type mRNA
#residues 1-212 #label MAY
#cross-references GB:M14584; NID:gl84628; PIDN:AAA52728.1; PID:g306910
REFERENCE I52193
#authors Wong, G.G.; Witek-Glannotti, J.; Hewick, R.M.; Clark, S.C.;
Ogawa, M.
#journal Behring Inst. Mitt. (1988) 83:40-47
#title Interleukin 6: Identification as a hematopoietic
colony-stimulating factor.
#cross-references MUID:89193317
#accession I52193
#status preliminary; translated from GB/EMBL/DDBJ
#molecule_type mRNA
#residues 1-212 #label WON
#cross-references GB:M54894; NID:gl86351; PIDN:AAC41704.1; PID:gl86352
REFERENCE I56003
#authors Brakenhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.;
Aarden, L.A.
#journal J. Immunol. (1987) 139:4116-4121
#title Molecular cloning and expression of hybridoma growth factor
in Escherichia coli.
#cross-references MUID:88088768
#accession I56003
#status translated from GB/EMBL/DDBJ
#molecule_type mRNA
```

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##residues      1-212 #label BRA
##cross-references GB:M18403; NID:g184631; PIDN:AAA52729.1; PID:g306911
REFERENCE
#authors      Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De
               Ley, M.; Billiau, A.
#journal      J. Immunol. (1988) 140:1534-1541
#title        Separation and comparison of two monokines with
               lymphocyte-activating factor activity: IL-1-beta and
               hybridoma growth factor (HGF). Identification of
               leukocyte-derived HGF as IL-6.
#cross-references MUID:88154445
#accession    A27601
##molecule_type protein
##residues    28-51,'X',53-57,'X',59,'X',61 #label VANI
#accession    B27601
##molecule_type protein
##residues    30-56,'XX',59-61,'X',63 #label VA2
REFERENCE
#authors      Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
               J. Immunol. (1990) 144:1808-1816
#journal      The human lung fibroblast cell line, MRC-5, produces multiple
               factors involved with megakaryocytopoiesis.
#title        Factors involved with megakaryocytopoiesis.
#cross-references MUID:90171574
#accession    A60400
##molecule_type protein
##residues    30-43 #label YAM
REFERENCE
#authors      Hirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.;
               Takatsuki, F.; Shimizu, M.; Murashima, A.; Tsunasawa, S.;
               Sakiyama, F.; Kishimoto, T.
               Proc. Natl. Acad. Sci. U.S.A. (1987) 84:228-231
#journal      Human beta-cell differentiation factor defined by an
               anti-peptide antibody and its possible role in autoantibody
               production.
#title        Human beta-cell differentiation factor defined by an
               anti-peptide antibody and its possible role in autoantibody
               production.
#cross-references MUID:87092370
#accession    A29085
##molecule_type protein
##residues    29-42 #label HIR2
REFERENCE
#authors      Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.;
               Hara, T.; Ishikawa, H.; Arimura, H.; Konno, K.
               Anticancer Res. (1991) 11:961-968
#journal      Purification and characterization of human fibroblast derived
               differentiation inducing factor for human monoblastic
               leukemia cells identical to interleukin-6.
#title        Purification and characterization of human fibroblast derived
               differentiation inducing factor for human monoblastic
               leukemia cells identical to interleukin-6.
#cross-references MUID:91290785
#accession    A61159
##molecule_type protein
##residues    30-42 #label NOD
##experimental_source fibroblast
REFERENCE
#authors      Ming, J.E.; Cernetti, C.; Steinman, R.M.; Granelli-Piperno,
               A.
               J. Mol. Cell. Immunol. (1989) 4:203-212
#journal      Interleukin 6 is the principal cytolytic T lymphocyte
               differentiation factor for thymocytes in human leukocyte
               conditioned medium.
#title        Interleukin 6 is the principal cytolytic T lymphocyte
               differentiation factor for thymocytes in human leukocyte
               conditioned medium.
#cross-references MUID:90121567
#accession    A61462
##molecule_type protein
##residues    28-48 #label MIN
##experimental_source leukocyte-conditioned medium
REFERENCE
#authors      May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriskie, J.B.; Sehgal,
               P.B.
               Cytokine (1991) 3:204-211
#journal      Marked cell-type-specific differences in glycosylation of
               human interleukin-6.
#title        Marked cell-type-specific differences in glycosylation of
               human interleukin-6.
#cross-references MUID:91355644
#accession    A48419
##molecule_type protein
##residues    30-37,'X',39-40 #label MAY2
##experimental_source FS-4 fibroblasts

```

```

##note      sequence extracted from NCBI backbone
##note      this 28-30K form contained both N-linked and O-linked
               carbohydrate; a 25K form containing only N-linked
               carbohydrate was also found
#accession    C48419
##molecule_type protein
##residues    28-40 #label MAY3
##experimental_source FS-4 fibroblasts
##note      sequence extracted from NCBI backbone (NCBIP:63787)
##note      this 23-25K form contained O-linked but not N-linked
               carbohydrate
REFERENCE
#authors      JX0305
               Orita, T.; Oheda, M.; Hasegawa, M.; Kuboniwa, H.; Esaki, K.;
               Ochi, N.
               J. Biochem. (1994) 115:345-350
#journal      Polypeptide and carbohydrate structure of recombinant human
               interleukin-6 produced in chinese hamster ovary cells.
#title        Polypeptide and carbohydrate structure of recombinant human
               interleukin-6 produced in chinese hamster ovary cells.
#cross-references MUID:94266765
#contents    annotation; modified sites in recombinant protein from CHO
               cells
REFERENCE
#authors      S04981
               Note: remainder of annotations omitted.
Query Match      33.8%; Score 1287; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.14e-225;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 29 PVPFGESKDVAAAPHRQPLTSSERIDKQIRYILDGTSALRKETCNKSNMCESSKEALAE 88
|||||
QY 342 PVPFGESKDVAAAPHRQPLTSSERIDKQIRYILDGTSALRKETCNKSNMCESSKEALAE 401
|||||
Db 89 NLNLPKMAERKDCGFCQSGFNEETCLVKITGLLEFVYLVYLNRFESSEQARAVQMSK 148
|||||
QY 402 NLNLPKMAERKDCGFCQSGFNEETCLVKITGLLEFVYLVYLNRFESSEQARAVQMSK 461
|||||
Db 149 VLIQFLQKKAKNLDAITTPDPTTNASLLTKLQANQWLDQMTTHILRSKFQSSLR 208
|||||
QY 462 VLIQFLQKKAKNLDAITTPDPTTNASLLTKLQANQWLDQMTTHILRSKFQSSLR 521
|||||
Db 209 LRQM 212
|||||
QY 522 LRQM 525
|||||
RESULT 5
ENTRY A37986 #type complete
TITLE interleukin-6 receptor precursor - rat
ALTERNATE_NAMES IL-6 receptor
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
22-Jun-1999
ACCESSIONS A37986
REFERENCE A37986
#authors Baumann, M.; Baumann, H.; Fey, G.H.
#journal J. Biol. Chem. (1990) 265:19853-19862
#title Molecular cloning, characterization and functional expression
               of the rat liver interleukin 6 receptor.
#cross-references MUID:91060602
#accession A37986
##molecule_type mRNA
##residues 1-462 #label BAU
##cross-references GB:M58587; GB:J05668; NID:g204921; PIDN:AAA41431.1;
               PID:g204922
COMMENT After binding IL-6, this chain associates with a 130K glycoprotein
               that is essential for transmembrane signaling.
CLASSIFICATION #superfamily ciliary neurotrophic factor receptor; cytokine
               receptor homology; immunoglobulin homology
KEYWORDS acute phase; cytokine receptor; transmembrane protein
FEATURE
1-19 #domain signal sequence #status predicted #label SIG\
20-462 #product interleukin-6 receptor #status predicted #label
               MAT\

```

```
20-362      #domain extracellular #status predicted #label EXT\
40-94      #domain immunoglobulin homology #label IMM\
117-306    #domain cytokine receptor homology #label CRS\
363-385    #domain transmembrane #status predicted #label TM\
386-462    #domain intracellular #status predicted #label IN\
47-92      #disulfide_bonds #status predicted
SUMMARY    #length 462 #molecular-weight 49560 #checksum 9669

Query Match      28.7%; Score 1090; DB 1; Length 462;
Best Local Similarity 51.1%; Pred. No. 2.93e-185;
Matches 167; Conservative 57; Mismatches 93; Indels 10; Gaps 6;

Db 1 MLAVGCTLLVALLAVALVGLSCRALEVANGTVTSLPGATVTLICFCGEAAGNATHW 60
Qy 1 MLAVGALLAALLAAGAALAPRCAPQAEVARGVLTSLPGDSVTLTCPGVEPDNATVHW 60
Db 61 VY----SCSQSEWTTGNTVLRAVQNDGCHYLCLFDDHLVGVPLLVDPPEPKLS 116
Qy 1 VLRKPAAGSHPSRWAGMRLLRSVQLHDSGNYSCYRAGRPAQVTHLLVDVPPPEPQLS 120
Db 117 CFRKNPLVNAFCWHPSTPPTTKAVMFAKKINTNGKSDFOVPCQYXSOQLKSFSCVE 176
Qy 121 CERKSPFNVCWGPSTPSTLTTRAVLLVRFQNSPAE-DQEPFCQYXSOQKFSQOLA 179
Db 177 ILEGKVVHYISLVANSVGRSSHNVFQSLKVMQPPPPANLVVSAIPGSLVGSKSYGK 236
Qy 180 VPEGDSFVIYVMCVASSVSGSKFTQTFQGGIILQPPANITVAVARNPR-WLSVTW 238
Db 237 TLPSTQVTTCCNSFDDLYGQR--TTVWPLQVACHOCVHDALRGVKKVHVQVGRKEE 294
Qy 239 Q-DPHSMNSSFYRLRFELRYAERSKTFTTWMVKDLQHCHVHDWSGLRHVYQLRAQEE 297
Db 295 PDIGOWSKSPREVTCPTWLAEPRTTPA 321
Qy 298 FQGESEWSPAMGTPW-TESRSPPA 323

RESULT      6
ENTRY      T09216      #type complete
TITLE      interleukin-6 precursor - horse
ORGANISM   #formal_name Equus caballus #common_name domestic horse
DATE       11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change
23-Jul-1999
ACCESSIONS T09216
REFERENCE   216613
#authors   Swiderski, C.E.; Horohov, D.W.
#submission submitted to the EMBL Data Library, July 1996
#accession T09216
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-208 #label SWI
#cross-references EMBL:U64794; NID:g2654387; PID:g2654388
GENETICS
#gene      IL-6
#superfamily interleukin-6
#keywords  cytokine; growth factor
SUMMARY    #length 208 #molecular-weight 23419 #checksum 3370

Query Match      21.2%; Score 806; DB 2; Length 208;
Best Local Similarity 59.2%; Pred. No. 2.88e-128;
Matches 109; Conservative 42; Mismatches 29; Indels 4; Gaps 3;

Db 29 PLPLGED--E-TTNSGPLLTTADTKQHKYTLGKISALKNMCMNFKSCNSKEVLAEN 85
Qy 342 PVPGEDSKDVAAPHRQPLTSERIDKQIRYILDGIGSALRKETCNKSNCSKEALAEAN 401
Db 86 NLNLPKMAEKDGCFCGSGFNOETCLMKITTLGSEFQYILEYQNERFGEKENIKTMQISTK 145
Qy 402 NLNLPKMAEKDGCFCGSGFNEETCLVKIITGLLEFEVLEYLQNERFESSEEQARAVQMTK 461
Db 146 VLVIQILQMKKNPE-VTTTPDPTAKSSLAKLHSONEWLKNFTTHILRSLEDFLOFSIRA 204
Qy 462 VLIIQFLQKAKNLDAITTPDPTTNASLLTKLQAQNWQLQDMTTHILRSFEFLQSSLRA 521
```

```
Db 205 VRIM 208
Qy 522 LRQM 525

RESULT      7
ENTRY      I46590      #type complete
TITLE      interleukin 6 - pig
ORGANISM   #formal_name Sus scrofa domestica #common_name domestic pig
DATE       21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
16-Jul-1999
ACCESSIONS I46590
REFERENCE   146590
#authors   Mathialagan, N.; Bixby, J.; Roberts, M.R.
#journal   Mol. Reprod. Dev. (1992) 32:324-330
#title     Expression of interleukin-6 in porcine, ovine, and bovine
           preimplantation conceptuses.
#cross-references MUID:92360284
#accession I46590
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-212 #label MAT
#cross-references GB:M80258; NID:g164514; PID:AAC27127.1; PID:g164515
GENETICS
#gene      IL-6
#superfamily interleukin-6
#keywords  cytokine; growth factor
SUMMARY    #length 212 #molecular-weight 23952 #checksum 759

Query Match      21.1%; Score 801; DB 2; Length 212;
Best Local Similarity 59.8%; Pred. No. 2.85e-127;
Matches 107; Conservative 37; Mismatches 35; Indels 0; Gaps 0;

Db 34 EDAKGDATSDKMLFTSPDKTEELIKYILKISAMKEMCEKEKCNSEKVEIAENNLNP 93
Qy 347 EDSKDVAAPHRQPLTSERIDKQIRYILDGIGSALRKETCNKSNCSKEALAEANLNP 406
Db 94 KMAEKDGCFCGSGFNOETCLMKITTLGVEFQYILDYLOKVEYKNGKVEAVQSTKALIQ 153
Qy 407 KMAEKDGCFCGSGFNEETCLVKIITGLLEFEVLEYLQNERFESSEEQARAVQMTKVLQF 466
Db 154 LRQKGNPKDATTPTNPTNAGLLDKLQSQNEWKNKTKIILIRSLRDFLOFSLRATRM 212
Qy 467 LQKAKNLDAITTPDPTTNASLLTKLQAQNWQLQDMTTHILRSFEFLQSSLRALRQM 525

RESULT      8
ENTRY      I46621      #type complete
TITLE      prointerleukin 6 - pig
ORGANISM   #formal_name Sus scrofa domestica #common_name domestic pig
DATE       21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
16-Jul-1999
ACCESSIONS I46621
REFERENCE   146621
#authors   Richards, C.; Saklatva, J.
#journal   Cytokine (1991) 3:269-276
#title     Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA
           and Expression of mRNA in Synovial Fibroblasts In Vitro.
#cross-references MUID:91338547
#accession I46621
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-212 #label RIC
#cross-references GB:M86722; NID:g164624; PID:AAC37333.1; PID:g164625
GENETICS
#gene      IL6
#superfamily interleukin-6
#keywords  cytokine; growth factor
SUMMARY    #length 212 #molecular-weight 23880 #checksum 819

Query Match      21.1%; Score 801; DB 2; Length 212;
Best Local Similarity 59.8%; Pred. No. 2.85e-127;
Matches 107; Conservative 37; Mismatches 35; Indels 0; Gaps 0;
```

```

Db 34 EDAGDATSKMLFTSPDKTEELIKYILGKISAMRKEMCEKYEKCNSEKVEIANNLNP 93
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 347 EDSKDVAAHPHQPTSSERIDKQIRYILGDISALRKETCNKSNMCESSKALAEANNLNP 406
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 94 KMAEKDCGFCGSGFNOETCLMRITGLVEFOIYLDYQKEYESKNGNVAEVOISTKALIQ 153
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 407 KMAEKDCGFCGSGFNEETCLVKIITGLLEFEVLEYLQNRFESEEQARAVQMSTKVLQ 466
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 154 LRQKGNPDKATTPNTTNAAGLLDKLOSQNEWMKNTKIILILRSLEDLFQFSRAIRIM 212
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 467 LQKAKNLDATTPDPTTNASLLTKLAQONQWLQDMTHILRSFKEFLQSSLRALROM 525
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
ENTRY #type complete
TITLE interleukin-6 precursor - bovine
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
ACCESSIONS A56610; S22162
REFERENCE A56610
#authors Droogmans, L.; Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.
#journal DNA Seq. (1992) 2:411-413
#title Nucleotide sequence of bovine interleukin-6 cDNA.
#cross-references MUID:93076003
#accession A56610
#status preliminary
#molecule_type mRNA
#residues 1-208 ##label DRO
#cross-references EMBL:X57317; NID:g2193; PIDN:CAA40572.1; PID:g2194
#experimental_source BLV induced B cell-lymphosarcoma
#note sequence extracted from NCBI backbone (NCBIP:118917)
CLASSIFICATION #superfamily interleukin-6
KEYWORDS cytokine
SUMMARY #length 208 #molecular_weight 23758 #checksum 8010

Query Match 18.2%; Score 693; DB 1; Length 208;
Best Local Similarity 51.1%; Pred. No. 6.67e-106;
Matches 93; Conservative 46; Mismatches 39; Indels 4; Gaps 2;

Db 29 PGLGEDFKNDTTPGRLLLTTPKEALIKRMVDKISAMRKEICEKNDCESSKETLAEN 88
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 342 PVPPECKDVAAHPHQPTSSERIDKQIRYILGDISALRKETCNKSNMCESSKALAE 401
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 89 KNLPMKEKDCGFCGSGFNOETCLMRITGLVEFOIYLDYQKEYESKNGNVAEVOISTK 148
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 402 NLNPKMAEKDCGFCGSGFNEETCLVKIITGLLEFEVLEYLQNRFESEEQARAVQMST 461
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 149 TLQILKOKIADL--ITTP--ATNTDLLEKMQSSNEWYKNAKIILILRNLENFLQFS 204
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 462 VLIQFLQKAKNLDATTPDPTTNASLLTKLAQONQWLQDMTHILRSFKEFLQSSLR 521
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 205 IR 206
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 522 LR 523

RESULT 10
ENTRY #type complete
TITLE interleukin 6 - cat
ORGANISM #formal_name Felis silvestris catus #common_name domestic cat
DATE 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change
ACCESSIONS I46084
REFERENCE I46084
#authors Bradley, W.G.; Gibbs, C.; Kraus, L.; Good, R.A.; Day, N.K.
#journal Proc. Soc. Exp. Biol. Med. (1993) 204:301-305
#title Molecular cloning and characterization of a cDNA encoding feline interleukin-6.
#cross-references MUID:94052249
#accession I46084
#status preliminary; translated from GB/EMBL/DBJ

```

```

#molecule_type mRNA
#residues 1-207 ##label BRA
#cross-references GB:L16914; NID:g438519; PIDN:AAAL6620.1; PID:g438520
CLASSIFICATION #superfamily interleukin-6
SUMMARY #length 207 #molecular_weight 23212 #checksum 9069

Query Match 17.9%; Score 680; DB 2; Length 207;
Best Local Similarity 52.3%; Pred. No. 2.40e-103;
Matches 91; Conservative 41; Mismatches 39; Indels 3; Gaps 2;

Db 36 ATSNRLPLPADKMEELIKYILGKISALKEKMDNTNKCDESKALAEANNLNPKLAEKD 95
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 353 AAPHRQPLTSSERIDKQIRYILGDISALRKETCNKSNMCESSKALAEANNLNPKMAEK 412
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 96 GCFQSGFNQETCLTRITTTGLOEFOIYILKFLQDKEYEGKNAKSVTSTNVLLQMLKRGK 155
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 413 GCFQSGFNEETCLVKIITGLLEFEVLEYLQNRFESEEQARAVQMSTKVLQFLQKAK 472
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 156 NQDEVTIPVPTVEVGL--QLCSHRRVAEAAHNNHLLTTLRLEDFLOLRRAVRIM 207
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 473 NLDAITTPDPTTNASLLTKLAQONQWLQDM--TTHLILRSFKEFLQSSLRALROM 525
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
ENTRY #type complete
TITLE interleukin-6 - sheep
ORGANISM #formal_name Ovis orientalis aries, Ovis ammon aries
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
ACCESSIONS S29549
REFERENCE S29549
#authors Ebrahimi, B.
#submission submitted to the EMBL Data Library, October 1992
#accession S29549
#status preliminary
#molecule_type mRNA
#residues 1-208 ##label EBR
#cross-references EMBL:X68723
CLASSIFICATION #superfamily interleukin-6
SUMMARY #length 208 #molecular_weight 23526 #checksum 7927

Query Match 17.9%; Score 679; DB 1; Length 208;
Best Local Similarity 50.5%; Pred. No. 3.78e-103;
Matches 92; Conservative 43; Mismatches 43; Indels 4; Gaps 2;

Db 29 PGLGEDFKNDTTPSRLLLTTPKEALIKHIVDKISAIRKEICEKNDCESSKETLAEN 88
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 342 PVPPECKDVAAHPHQPTSSERIDKQIRYILGDISALRKETCNKSNMCESSKALAE 401
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 89 KKLKLPKMEKDCGFCGSGFNOAVCLIKTTAGLLEYQIYLDLQNEFQNETVWELQSSIR 148
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 402 NLNPKMAEKDCGFCGSGFNEETCLVKIITGLLEFEVLEYLQNRFESEEQARAVQMST 461
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 149 TLQILKEKTAGL--ITTP--ATHTDLLEKMQSSNEWYKNAKVIIILRSLENFLQFLRA 204
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 462 VLIQFLQKAKNLDATTPDPTTNASLLTKLAQONQWLQDMTHILRSFKEFLQSSLR 521
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 205 IR 206
  ||| 1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 522 LR 523

RESULT 12
ENTRY #type complete
TITLE interleukin-6 precursor - mouse
ALTERNATE_NAMES B-cell hybridoma growth factor; B-cell stimulating factor 2;
hepatocyte-stimulating factor; IL-6; interferon beta-II;
interleukin-HPI; myeloid differentiation inducer MGI-2A;
plasmacytoma growth factor
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change
22-Jun-1999

```

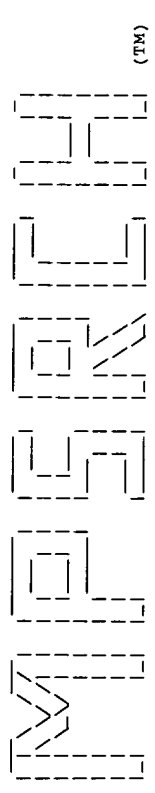
ACCESSIONS A30531; A27610; A30571; S01323; S12103; E34047; A26662;
 REFERENCE A40486; A60799; S10241; S38254
 #authors Tanabe, O.; Akira, S.; Kamiya, T.; Wong, G.G.; Hirano, T.;
 #journal Kishimoto, T.
 #title J. Immunol. (1988) 141:3875-3881
 #cross-references Genomic structure of the murine IL-6 gene. High degree
 conservation of potential regulatory sequences between
 mouse and human.
 #accession A30531
 #molecule_type mRNA
 #residues 1-211 ##label TAN
 #cross-references GB:M20572; PIDN:AAA39302.1; PID:g387386
 REFERENCE A27610
 #authors Van Snick, J.; Cayphas, S.; Szikora, J.P.; Renauld, J.C.; Van
 Roost, E.; Boon, T.; Simpson, R.J.
 #journal Eur. J. Immunol. (1988) 18:193-197
 #title cDNA cloning of murine interleukin-6.
 #cross-references MUID:88166883
 #accession A27610
 #molecule_type mRNA
 #residues 1-211 ##label VAN
 #cross-references GB:X06203; NID:g52701; PIDN:CAA29560.1; PID:g52702
 REFERENCE A30571
 #authors Mock, B.A.; Nordan, R.P.; Justice, M.J.; Kozak, C.; Jenkins,
 N.A.; Copeland, N.G.; Clark, S.C.; Wong, G.G.; Rudikoff, S.
 #journal J. Immunol. (1989) 142:1372-1376
 #title The murine IL-6 gene maps to the proximal region of
 chromosome 5.
 #cross-references MUID:89124383
 #accession A30571
 #molecule_type mRNA
 #residues 5-211 ##label MOC
 #cross-references GB:M24221; NID:g341131; PIDN:AAA68814.1; PID:g870699
 REFERENCE S01323
 #authors Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.
 #journal Eur. J. Biochem. (1988) 176:187-197
 #title Murine hybridoma/plasmacytoma growth factor. Complete
 amino-acid sequence and relation to human interleukin-6.
 #cross-references MUID:88329059
 #accession S01323
 #molecule_type protein
 #residues 25-166,'X',168-211 ##label SIM
 #note the sequence from Fig. 11 is inconsistent with that from
 Fig. 10 in having 103-Asn
 REFERENCE S12103
 #authors Grenett, H.E.; Fuentes, N.L.; Fuller, G.M.
 #journal Nucleic Acids Res. (1990) 18:6455
 #title Cloning and sequence analysis of the cDNA for murine
 interleukin-6
 #cross-references MUID:91057159
 #accession S12103
 #molecule_type mRNA
 #residues 1-211 ##label GRE
 #cross-references EMBL:X54542; NID:g52727; PIDN:CAA38411.1; PID:g52728
 REFERENCE A90157
 #authors Jahnén, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson,
 R.J.
 #journal Biochem. Biophys. Res. Commun. (1990) 166:139-145
 #title Internal amino acid sequencing of proteins by in situ
 cyanogen bromide cleavage in polyacrylamide gels.
 #cross-references MUID:90147691
 #accession E34047
 #molecule_type protein
 #residues 66-69,'X',71-75;78-94;128-148 ##label JA5
 REFERENCE A26662
 #authors Van Snick, J.; Cayphas, S.; Vink, A.; Uyttenhove, C.; Coulie,
 P.G.; Rubira, M.R.; Simpson, R.J.
 #journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:9679-9683
 #title Purification and NH2-terminal amino acid sequence of a
 T-cell-derived lymphokine with growth factor activity for

B-cell hybridomas.
 #cross-references MUID:87092311
 #accession A26662
 #molecule_type protein
 #residues 25-39,'X',41-42,'X',44-45 ##label VSN
 REFERENCE A40486
 #authors Chiu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.
 #journal Proc. Natl. Acad. Sci. U.S.A. (1988) 85:7099-7103
 #title Multiple biological activities are expressed by a mouse
 interleukin 6 cDNA clone isolated from bone marrow stromal
 cells.
 #cross-references MUID:89017145
 #accession A40486
 #molecule_type mRNA
 #residues 1-211 ##label CHI
 #cross-references GB:J03783; NID:g198367; PIDN:AAA39301.1; PID:g309410
 REFERENCE A60799
 #authors Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.;
 Wolf, S.F.; Kamen, R.; Sachs, L.
 #journal Blood (1988) 72:2070-2073
 #title The myeloid blood cell differentiation-inducing protein
 MGI-2A is interleukin-6.
 #cross-references MUID:89062753
 #accession A60799
 #molecule_type protein
 #residues 77-98 ##label SHA
 REFERENCE S10241
 #authors Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
 #journal J. Exp. Med. (1990) 171:965-970
 #title DNA rearrangement and constitutive expression of the
 interleukin 6 gene in a mouse plasmacytoma.
 #cross-references MUID:90171860
 #accession S10241
 #status preliminary
 #molecule_type DNA
 #residues 1-6 ##label BLA
 #cross-references EMBL:X51457; NID:g49738; PIDN:CAA35824.1; PID:g581860
 REFERENCE S38254
 #authors Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson,
 R.J.
 #journal Eur. J. Biochem. (1993) 217:53-59
 #title Specific covalent modification of the tryptophan residues in
 murine interleukin-6. Effect on biological activity and
 conformational stability.
 #cross-references MUID:94039075
 #accession S38254
 #status preliminary
 #molecule_type protein
 #residues 38-60;75,'X',77-79;176-203 ##label ZHA
 GENETICS
 #gene Il-6
 #map_position 5
 #introns 7/1; 68/3; 106/3; 156/3
 CLASSIFICATION #superfamily interleukin-6
 KEYWORDS Castleman's disease; cytokine; growth factor;
 immunoregulation; lymphokine; macrophage; rheumatoid
 arthritis
 FEATURE
 1-24 #domain signal sequence #status predicted #label SIG\
 25-211 #product interleukin-6 #status experimental #label MAT
 SUMMARY #length 211 #molecular-weight 24384 #checksum 5652
 Query Match 14.7%; Score 560; DB 1; Length 211;
 Best Local Similarity 40.4%; Pred. No. 6.17e-80;
 Matches 74; Conservative 50; Mismatches 56; Indels 3; Gaps 3;
 Db 30 VRRGDTED-TTPNR-PVYTTTSOVGGLTHVLWEIVEMKELCNGNSDCMNNDDALAENN 87
 Qy 343 VPPGDSKDVRAAPHQPTTSERIDKQIRYILDGTSALRKETCNKSNMCESSKEALAENN 402
 Db 88 LKLPRIQRNDGQYQYNGEICLLKISSGLLEYSHLYEYMKNNLKNKDKARVLQRDTE 147
 Qy 403 LNLPMKAEKDCGFCQSFNEETCLVKIITGLLEFFELYEYVLYLQNRFF-ESSEEQARAVQMSTK 461


```
#journal      Genomics (1995) 25:157-163
#title        Genomic organization and chromosomal localization of the
              human and mouse genes encoding the alpha receptor component
              for ciliary neurotrophic factor.
#cross-references MUID:95293367
#accession    A56526
#molecule_type DNA
##residues    1-346, 'S', 348-372 #label VAL
##cross-references GB:138025; NID:g608654; PIDN:AAA91337.1; PID:g608656
COMMENT       The CNTF receptor is attached to the membrane by a
              glycosylphosphatidylinositol anchor.
COMMENT       The CNTF receptor sequence appears to contain several PEST regions.
GENETICS
#gene         GDB:CNTRF
##cross-references GDB:134652; OMIM:118946
#map.position 9p13-9p13
CLASSIFICATION #superfamily ciliary neurotrophic factor receptor; cytokine
              receptor homology; immunoglobulin homology
KEYWORDS       glycoprotein; growth factor receptor; membrane protein;
              phosphatidylinositol linkage
FEATURE
1-20           #domain signal sequence #status predicted #label SIG\
21-372         #product ciliary neurotrophic factor receptor #status
              predicted #label MAT\
39-91          #domain immunoglobulin homology #label IMM\
116-296        #domain cytokine receptor homology #label CRS\
46-89          #disulfide_bonds #status predicted\
60,70,142,190 #binding_site carbohydrate (Asn) (covalent) #status
              predicted
SUMMARY        #length 372 #molecular-weight 40649 #checksum 6224
Query Match    10.6%; Score 403; DB 1; Length 372;
Best Local Similarity 31.7%; Pred. No. 4 60e-50;
Matches 99; Conservative 75; Mismatches 115; Indels 23; Gaps 20;
Db 11 AVLAATAAVVYAAQRHSPQAPHVQYERL-GSDVTLPC-GT-ANWDAAVTW--RVNGTDLA 65
QY 11 ALTAAPGAALAPRCAPQAEVARGVLTSLPGDSVTLTCPGVEPEDNATVHWLKRPAAGSH 70
Db 66 PLLNG-SQ-LVLHGLEHSGLYACFHRDWSHLRHVLLHYGLPPREPVLSC-RSNTYP 122
QY 71 PSRWAGMRRLRLRSVQLHDSNYSICY-RAGRPAGTVHLL-VDPPEEPQLSCFRKSPUS 128
Db 123 KGFYCSW-HLPTPTYIPNT-FNVTVLHGS---KINV-CE-KDPALKNRCHIRYMHLFSTI 175
QY 129 NVV-CEWGRSTPSLTTRAVLLVRKFQNSPAEDFQPCQYSQESQKFSQCLAVPECDSSF 187
Db 176 KYKVISVSNALGHN-ATAITDEFETIVKDPDENNVARVPVPSNPRRLEVTWQTPSTWPD 234
QY 188 -YIVSMCVASSYGSFKSTQTQGGGILQPPPPANITVTAVARNPRLSVTWQDPHSW-N 245
Db 235 PESEPLKEFLRYRPLLDQWQHVELSDGTAH-TITDAVAGKEYIIIOVAAKDN-EIGTWSD 292
QY 246 SSFYRLRELFYRAERSKFTFTTMVMDLQHCVIHDWSGLRHVVOLRAQEFGQGEWSE 305
Db 293 WSAVAHAATPWTE 304
QY 306 WSPKAMGTPWTE 317
```

Search completed: Thu Aug 10 16:01:39 2000
Job time : 83 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Aug 10 16:06:14 2000; MasPar time 10.61 Seconds
Tabular output not generated. 714.244 Million cell updates/sec

Title: >US-09-142-471-2
Description: (1-525) from US09142471.pep
Perfect Score: 3803
Sequence: 1 MLAVGCCALLAALAPGAAL.....LILRSKFELQSSLRALRQM 525

Scoring table: PAM 150
Gap 11

Searched: 145341 seqs, 14437480 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Statistics: Mean 35.092; Variance 199.930; scale 0.176

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2398	63.1	344	5	5480796-7	5.13e-167
2	2398	63.1	344	5	5171840-7	5.13e-167
3	2398	63.1	468	5	5480796-2	5.13e-167
4	2398	63.1	468	5	5171840-2	5.13e-167
5	2394	63.0	323	5	5480796-6	1.03e-166
6	2394	63.0	323	5	5171840-6	1.03e-166
7	1542	40.5	386	5	5480796-5	9.46e-103
8	1542	40.5	386	5	5171840-5	9.46e-103
9	1339	35.2	317	4	PCT-US95-0	Sequence 145, Applicat
10	1339	35.2	317	3	US-08-469-	Sequence 145, Applicat
11	1306	34.3	201	5	5171840-11	3.94e-85
12	1289	33.9	186	4	PCT-US94-1	Sequence 20, Applicati
13	1289	33.9	186	3	US-08-469-	Sequence 163, Applicat
14	1289	33.9	186	1	US-08-165-	Sequence 20, Applicati
15	1289	33.9	186	1	US-07-921-	Sequence 20, Applicati
16	1289	33.9	186	4	PCT-US95-0	Sequence 163, Applicat
17	1289	33.9	186	1	US-07-632-	Sequence 20, Applicati
18	1289	33.9	186	1	US-07-745-	Sequence 20, Applicati
19	1287	33.8	184	2	US-08-567-	Sequence 2, Applicatio
20	1287	33.8	184	1	US-08-567-	Sequence 2, Applicatio
21	1287	33.8	184	5	5186931-1	Sequence 2, Applicatio
22	1287	33.8	185	1	US-07-918-	Sequence 2, Applicatio
23	1287	33.8	185	1	US-08-246-	Sequence 5, Applicatio

RESULT	ID	5480796-7	STANDARD;	PRT;	344 AA.
XX	AC	xxxxxx			
XX	DT				
XX	DE	Patent No. 5480796			
XX	DE	Patent No. 5480796			
CC	CC	APPLICANT: KISHIMOTO, TADAMITSU			
CC	CC	TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN			
CC	CC	FOR HUMAN B CELL STIMULATORY FACTOR-2			
CC	CC	NUMBER OF SEQUENCES: 8			
CC	CC	CURRENT APPLICATION DATA:			
CC	CC	APPLICATION NUMBER: US/07/907,650			
CC	CC	FILING DATE: 02-JUL-1992			
CC	CC	PRIOR APPLICATION DATA:			
CC	CC	APPLICATION NUMBER: 298,694			
CC	CC	FILING DATE: 19-JAN-1989			
CC	CC	SEQ ID NO:7:			
CC	CC	LENGTH: 344			
CC	CC	SEQUENCE 344 AA; 38047 MW; 637889 CN;			
ALIGNMENTS					
Query Match	63.1%	Score 2398;	DB 5;	Length 344;	
Best Local Similarity	100.0%	Pred. No. 5.13e-167;			
Matches	323;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
Db	1	MLAVGCCALLAALAPGAALAPRRCPAQEVARGLTSLPGDSVTLTCPGVEPNATVHW	60		
Qy	1	MLAVGCCALLAALAPGAALAPRRCPAQEVARGLTSLPGDSVTLTCPGVEPNATVHW	60		
Db	61	VLRKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSYCRAGRAGTAVHLLVDVPPPEPQLS	120		
Qy	61	VLRKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSYCRAGRAGTAVHLLVDVPPPEPQLS	120		
Db	121	CFRKSPLSNVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFQPCOYSQESKFKSCOLAV	180		
Qy	121	CFRKSPLSNVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFQPCOYSQESKFKSCOLAV	180		
Db	181	PEGSSFFIVSMCVASSVSGSKFSTQTGGCGILQDPDPANTVAVARNPRLSVTWQD	240		
Qy	181	PEGSSFFIVSMCVASSVSGSKFSTQTGGCGILQDPDPANTVAVARNPRLSVTWQD	240		
Db	241	PSHWNSSFYRLRFELRYRAERSKFTTVMWKDLQHCYVHDWAGSLRHVVQLRAQEFGQ	300		
Qy	241	PSHWNSSFYRLRFELRYRAERSKFTTVMWKDLQHCYVHDWAGSLRHVVQLRAQEFGQ	300		


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CC STRANDEDNESS:
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 317 AA: 35632 MW; 490978 CN;

Query Match 35.2%; Score 1339; DB 3; Length 317;
Best Local Similarity 97.5%; Pred. No. 1.37e-87;
Matches 192; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 121 SPGGSGGSGNMAPVPPGSDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKETCNKS 180
QY 329 SGGSGGGGSEVPVPPGSDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKETCNKS 388
Db 181 NCMESSKEALAEENNLNPKMAEKDCGFCGSGFNEETCLVKIITGLLEFEVLEYLQNRRES 240
QY 389 NCMESSKEALAEENNLNPKMAEKDCGFCGSGFNEETCLVKIITGLLEFEVLEYLQNRRES 448
Db 241 SEQARAVQMSTKVLQFLOKAKNLDAITTPDPTTNASLLTKLQAOQNWLDQMTTHLIL 300
QY 449 SEQARAVQMSTKVLQFLOKAKNLDAITTPDPTTNASLLTKLQAOQNWLDQMTTHLIL 508
Db 301 RSFKEFLQSSLRALROM 317
QY 509 RSFKEFLQSSLRALROM 525

RESULT 11
ID 5171840-11 STANDARD; PRT; 201 AA.
XX xxxxxx
DT
DE Patent No. 5171840
XX
CC Patent No. 5171840
CC APPLICANT: KISHIMOTO, TADAMITSU
CC TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
CC STIMULATORY FACTOR-2
CC NUMBER OF SEQUENCES: 11
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/298,694
CC FILING DATE: 19-JAN-1989
CC SEQ ID NO:11
CC LENGTH: 201
CC SEQUENCE 201 AA: 22672 MW; 223180 CN;

Query Match 34.3%; Score 1306; DB 5; Length 201;
Best Local Similarity 89.1%; Pred. No. 3.94e-85;
Matches 180; Conservative 4; Mismatches 16; Indels 2; Gaps 2;

Db 1 RKSPLSNVVCEWGRSTPSLTTKAVLLVRKFOQLAVPE-GDSSEFVIVSMCVASSVQLAVP 59
QY 123 RKSPLSNVVCEWGRSTPSLTTKAVLLVRKFOQNSPAEDFQPCQSQE-SOKFSCQLAVP 181
Db 60 EGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVTAVARNRWLSVTWQDP 119
QY 182 EGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVTAVARNRWLSVTWQDP 241
Db 120 HSWNSSFYLRPELRYAERSKFTFTVMVKDLQHCVITHDAWSGLRHVVVQLRAQEFQGG 179
QY 242 HSWNSSFYLRPELRYAERSKFTFTVMVKDLQHCVITHDAWSGLRHVVVQLRAQEFQGG 301
Db 180 EWSSESPAMGTPWTESRPPA 201
QY 302 EWSSESPAMGTPWTESRPPA 323

RESULT 12
ID PCT-US94-14179-20 STANDARD; PRT; 186 AA.
XX xxxxxx
AC xxxxxx
DT
XX
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DT
XX
DE Sequence 20, Application PC/TUS9414179
XX
CC Sequence 20, Application PC/TUS9414179
CC GENERAL INFORMATION:
CC APPLICANT: McCoy, John
CC APPLICANT: DiBlasio-Smith, Elizabeth
CC APPLICANT: Grant, Kathleen
CC APPLICANT: Lavallie, Edward R.
CC TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
CC TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
CC NUMBER OF SEQUENCES: 29
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genetics Institute, Inc.
CC STREET: 87 Bridgepark Drive
CC CITY: Cambridge
CC STATE: Massachusetts
CC COUNTRY: U.S.A.
CC ZIP: 02140
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/14179
CC FILING DATE:
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Meinerdt, M. C.
CC REGISTRATION NUMBER: 33,544
CC REFERENCE/DOCKET NUMBER: GI 5188D
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (617) 876-1170
CC TELEFAX: (617) 876-5851
CC INFORMATION FOR SEQ ID NO: 20:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 186 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 186 AA: 21112 MW; 171066 CN;

Query Match 33.9%; Score 1289; DB 4; Length 186;
Best Local Similarity 98.9%; Pred. No. 7.27e-84;
Matches 184; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MAPVPPGSDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKETCNKSNMCESSKEALA 60
QY 340 VEPVPPGSDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKETCNKSNMCESSKEALA 399
Db 61 ENNLNPKMAEKDCGFCGSGFNEETCLVKIITGLLEFEVLEYLQNRFESESEQARAVQMS 120
QY 400 ENNLNPKMAEKDCGFCGSGFNEETCLVKIITGLLEFEVLEYLQNRFESESEQARAVQMS 459
Db 121 TKVLQFLOKAKNLDAITTPDPTTNASLLTKLQAOQNWLDQMTTHLILRSFKEFLQSSL 180
QY 460 TKVLQFLOKAKNLDAITTPDPTTNASLLTKLQAOQNWLDQMTTHLILRSFKEFLQSSL 519
Db 181 RALROM 186
QY 520 RALROM 525

RESULT 13
ID US-08-469-318-163 STANDARD; PRT; 186 AA.
XX xxxxxx
AC xxxxxx
DT
XX
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CC ZIP: 02140
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/921,848
CC FILING DATE: 19920728
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/652,531
CC FILING DATE: 06-FEB-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/745,382
CC FILING DATE: 14-AUG-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Cserr, Luann
CC REGISTRATION NUMBER: 31,822
CC REFERENCE/DOCKET NUMBER: G15188A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (617) 876-1170
CC TELEFAX: (617) 876-5851
CC INFORMATION FOR SEQ ID NO: 20:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 186 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 186 AA; 21112 MW; 171066 CN;

Query Match 33.9%; Score 1289; DB 1; Length 186;
Best Local Similarity 98.9%; Pred. No. 7.27e-84;
Matches 184; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MAPVPPGSDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALA 60
Qy 340 VEPVPPGSDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALA 399
Db 61 ENNLNLPKMAEKDGCFSQGFNEETCLVKIITGLLEFEVYLEYLQNRFFESSEEQARAVOMS 120
Qy 400 ENNLNLPKMAEKDGCFSQGFNEETCLVKIITGLLEFEVYLEYLQNRFFESSEEQARAVOMS 459
Db 121 TKVLIQFLOKKAKNLDATTPDPTTNASLLTKLQAQONQWLQDMTTHLILRSFKFELQSSL 180
Qy 460 TKVLIQFLOKKAKNLDATTPDPTTNASLLTKLQAQONQWLQDMTTHLILRSFKFELQSSL 519
Db 181 RALROM 186
Qy 520 RALROM 525

Search completed: Thu Aug 10 16:07:05 2000
Job time : 51 secs.

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(TM)

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>US-09-142-471-2
Title:
Description:
Perfect Score: 3803
Sequence: 1 MIAVGCALLAALLAAPGAAL.....LIIRSFKEFIQSSRLRALRM 525
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Scoring table: PAM 150
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Database: a-geneseq36
          1:geneseqp
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Statistics: Mean 37.337; Variance 202.644; scale 0.184

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	No.	Score	Query Match %	Length	DB ID	Description	Pred. No.
1	3803	100.0	525	1	W36846	Human fusion polypepti	8-73e-28
2	3510	92.3	543	1	Y03164	Chimeric sIL-6R/IL-6 p	1.52e-26
3	3335	87.7	500	1	W36847	Human fusion polypepti	1.13e-24
4	2398	63.1	344	1	P90528	B cell stimulating fac	1.55e-17
5	2398	63.1	468	1	R37215	IL-6 receptor.	1.55e-17
6	2398	63.1	468	1	P90284	Sequence of a receptor	1.55e-17
7	2391	62.9	360	1	W07804	Amino acid sequence of	5.54e-17
8	2392	62.9	360	1	R98364	Interleukin-6 receptor	4.62e-17
9	2391	62.9	592	1	W07977	Human interleukin-6R-a	5.54e-17
10	2390	62.8	468	1	P90525	B cell stimulating fac	6.65e-17
11	2373	62.4	468	1	W11371	Human interleukin-6 re	1.46e-17
12	2351	61.8	323	1	P90527	B cell stimulating fac	7.97e-17
13	2317	60.9	315	1	W70805	Amino acid sequence of	3.85e-16
14	2110	55.5	1042	1	E70122	IL8-R type 1-GBP 130 f	8.14e-15
15	1534	40.3	386	1	P90526	B cell stimulating fac	1.55e-10
16	1368	36.0	182	1	W00403	Interleukin-6 antagoni	1.52e-93
17	1320	34.7	460	1	R22616	IL-6R for soluble IL-6	8.53e-90
18	1311	34.5	460	1	R13318	IL-6 receptor.	4.30e-89
19	1289	33.9	186	1	P80270	Recombinant interleuki	2.25e-87
20	1289	33.9	186	1	R75765	Human interleukin-6.	2.25e-87
21	1287	33.8	184	1	R03914	Polypeptide with human	3.22e-87
22	1287	33.8	184	1	R55256	Interleukin 6.	3.22e-87
23	1287	33.8	184	1	P81158	Polypeptide with B cel	3.22e-87

DR WPI; 97-470536/43.
DR N-PSDB; T97849.
PT Conjugate of two peptide(s) with mutual affinity connected by a
PT linker - used to modulate interactions between proteins, e.g. for ex
PT vivo expansion of human stem cells
PS Disclosure; Fig 2; 19pp; German.
CC This sequence represents the fusion polypeptide H-IL-6 which contains
CC an 13 amino acid linker which joins the carboxy terminus of human
CC interleukin-6 receptor (IL-6R) with the amino terminus of human
CC interleukin-6 (IL-6). Such conjugates could be used to modulate
CC interactions between proteins, particularly to overcome interrupted
CC interactions caused by an incomplete interleukin-6 (IL-6) receptor. These
CC constructs derived from IL-6 and its receptor, can also be used for ex
CC vivo expansion of human stem cells, and as a therapeutic IL-6 receptor
CC antagonist.
SQ Sequence 500 AA;

Query Match 87.7%; Score 3335; DB 1; Length 500;
Best Local Similarity 95.2%; Pred. No. 1.13e-248;
Matches 500; Conservative 0; Mismatches 0; Indels 25; Gaps 2;

Db 1 MLAVGCALLAALLAAGAAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
QY 1 MLAVGCALLAALLAAGAAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRAGTVHLLVDVPPPEPQLS 120
QY 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRAGTVHLLVDVPPPEPQLS 120
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSOESQKFCQLAV 180
QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSOESQKFCQLAV 180
Db 181 PGDSSFYIVSMCVASSVSGSKFTQTQFCGCGILOPDPANITVTAVARNRWLSVTWQD 240
QY 181 PGDSSFYIVSMCVASSVSGSKFTQTQFCGCGILOPDPANITVTAVARNRWLSVTWQD 240
Db 241 PHSNNSFYRLRFELRYRAERSKFTTWMVKDLQHHCYVHDAWSGLRHVQLRAQEEFGQ 280
QY 241 PHSNNSFYRLRFELRYRAERSKFTTWMVKDLQHHCYVHDAWSGLRHVQLRAQEEFGQ 300
Db 281 GEWSWSPAMGTPWTERSPARGGGGGGGG-----VEPVPGEDSKDVAAPHROPL 335
QY 301 GEWSWSPAMGTPWTERSPARGGGGGGGG-----VEPVPGEDSKDVAAPHROPL 360
Db 336 TSSERIDKQIRYILDGIGSALRKETCNKNCESSEKAEALNNLPKMAEKDGCQSGFN 395
QY 361 TSSERIDKQIRYILDGIGSALRKETCNKNCESSEKAEALNNLPKMAEKDGCQSGFN 420
Db 396 EETCLVKIITGLLEPEVYLEYQNRFESEEQARAVQMSKVLQFLOKAKNLDIAITTP 455
QY 421 EETCLVKIITGLLEPEVYLEYQNRFESEEQARAVQMSKVLQFLOKAKNLDIAITTP 480
Db 456 DPTTNASLLTKLQAOQWLDQMTTHLILRSKFEQLQSSILRALROM 500
QY 481 DPTTNASLLTKLQAOQWLDQMTTHLILRSKFEQLQSSILRALROM 525

RESULT 4
ID P90528 standard; protein; 344 AA.
AC P90528;
DT 25-JAN-1990 (first entry)
DE B cell stimulating factor-2 receptor.
KW B cell stimulating factor-2 receptor; monocytic U937 cell line.
OS Homo sapiens.
PN A08928720-A.
PD 27-JUL-1989.
PR 23-JAN-1989; 028720.
PR 22-JAN-1988; JP-012387.
PR 25-JAN-1988; JP-012599.
PR 04-AUG-1988; JP-194885.
PR 14-JAN-1989; JP-007461.
PA (KISH) Tadimitsu Kishimoto.

PI Kishimoto T;
DR WPI; 89-264012/37.
DR N-PSDB; P90525.
PT Receptor protein for human B cell stimulating factor-2 - used for
PT developing prophylactic, therapeutic and diagnostic agents for
PT associated disorders.
PS Claim 7; page 40; 76pp; English.
CC The Bsf2 receptor has amino acids at the C-terminal deleted. The receptor
CC is derived from a monocytic U937 cell line. It can be used to develop
CC prophylactic and therapeutic pharmaceuticals, as agents to relate
CC diseases and disorders to abnormal Bsf-2 prodn. It can also be used to
CC study an immune mechanism with which Bsf-2 or the receptor is concerned.
SQ Sequence 344 AA;

Query Match 63.1%; Score 2398; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.55e-174;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLAVGCALLAALLAAGAAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
QY 1 MLAVGCALLAALLAAGAAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRAGTVHLLVDVPPPEPQLS 120
QY 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRAGTVHLLVDVPPPEPQLS 120
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QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSOESQKFCQLAV 180
Db 181 PGDSSFYIVSMCVASSVSGSKFTQTQFCGCGILOPDPANITVTAVARNRWLSVTWQD 240
QY 181 PGDSSFYIVSMCVASSVSGSKFTQTQFCGCGILOPDPANITVTAVARNRWLSVTWQD 240
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QY 241 PHSNNSFYRLRFELRYRAERSKFTTWMVKDLQHHCYVHDAWSGLRHVQLRAQEEFGQ 300
Db 301 GEWSWSPAMGTPWTERSPPA 323
QY 301 GEWSWSPAMGTPWTERSPPA 323

RESULT 5
ID R37215 standard; Protein; 468 AA.
AC R37215;
DT 13-SEP-1993 (first entry)
DE IL-6 receptor.
KW Interleukin-6; IL-6; receptor; immunoglobulin-like; domain; truncated;
KW transmembrane; multiple myeloma; binding; ability; signal transfer;
KW disease; intracellular.
OS Synthetic.
PN J05091892-A.
PD 16-APR-1993.
PR 02-OCT-1991; 255521.
PR 02-OCT-1991; JP-255521.
PA (CHUS) CHUGAI PHARM CO LTD.
PA (KISH/) KISHIMOTO C.
PA (TOYJ) TOSOH CORP.
DR WPI; 93-161739/20.
DR N-PSDB; Q41746.
PT New interleukin-6 receptor deriv. - for treating diseases caused
PT by IL-6, e.g. multiple myeloma
PS Disclosure; Page 10-12; 23pp; Japanese.
CC This sequence represents an interleukin-6 (IL-6) receptor. Variants
CC of the receptor lacking either the immunoglobulin-like domain or the
CC transmembrane and intracellular domain have IL-6 binding ability and
CC signal transfer ability. Either the full length or truncated IL-6
CC receptors may be used for diseases caused by IL-6 such as multiple
CC myeloma.
SQ Sequence 468 AA;

Query Match 63.1%; Score 2398; DB 1; Length 468;


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Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFCGILQDPDPANITVTAVARNPRLSVTWQD 240
|||||
Qy 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFCGILQDPDPANITVTAVARNPRLSVTWQD 240
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Db 241 PHSWNSFFYRLRFELRYRAERSKFTTWMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300
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Qy 241 PHSWNSFFYRLRFELRYRAERSKFTTWMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300
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Db 301 GEWSEWSPAMGTPWTESRPPA 323
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Qy 301 GEWSEWSPAMGTPWTESRPPA 323
|||||

RESULT 8
ID R98364 standard; Protein; 468 AA.
AC R98364;
DT 28-NOV-1996 (first entry)
DE Interleukin-6 receptor.
KW gene expression; kidney tumour; myeloma; Kaposi's sarcoma; psoriasis;
KW rheumatoid arthritis; endotoxin shock.
OS Homo sapiens.
PN WO9618416-A1.
PD 20-JUN-1996.
PF 15-DEC-1995; J02587.
PR 16-DEC-1994; JP-313167.
PR 18-AUG-1995; JP-210739.
PA (CHUS) CHUGAI SEIYAKU KK.
PI Koishibara Y, Kuromaru K;
DR WPI; 96-300392/30.
DR N-PSDB; T31441.
PT Anti-sense oligo:nucleotide inhibitor against human IL-6R expression
PT - for treatment of e.g. tumours, cancers, rheumatoid arthritis,
PT psoriasis, endo:toxic shock, etc.
PS Claim 2; Page 17-21; 32pp; Japanese.
CC Antisense oligonucleotides may be used to inhibit the expression of
CC the interleukin-6 receptor. Inhibition of expression of the
CC IL-6 receptor is useful in the treatment of kidney tumours, myeloma,
CC Kaposi's sarcoma, rheumatoid arthritis, psoriasis and endotoxin
CC shock. The antisense oligonucleotides are administered at a dosage
CC of 0.1-100mg/kg, pref. 0.1-50 mg/kg.
SQ Sequence 468 AA;

Query Match 62.9%; Score 2392; DB 1; Length 468;
Best Local Similarity 99.7%; Pred. No. 4.62e-174;
Matches 322; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLAVGALLAALLAAPGAALAPRCRPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
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Qy 1 MLAVGALLAALLAAPGAALAPRCRPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
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Db 61 LLRKPAGSHPSRWAGMGRLLRSVQLHDSGNYSYRAGRAGTAVHLLVDVPPPEPQLS 120
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Qy 61 LLRKPAGSHPSRWAGMGRLLRSVQLHDSGNYSYRAGRAGTAVHLLVDVPPPEPQLS 120
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Qy 121 CRRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSOESQKFCQLAV 180
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Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFCGILQDPDPANITVTAVARNPRLSVTWQD 240
|||||
Qy 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFCGILQDPDPANITVTAVARNPRLSVTWQD 240
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Db 241 PHSWNSFFYRLRFELRYRAERSKFTTWMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300
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Qy 241 PHSWNSFFYRLRFELRYRAERSKFTTWMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300
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Db 301 GEWSEWSPAMGTPWTESRPPA 323
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Qy 301 GEWSEWSPAMGTPWTESRPPA 323
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RESULT 9
ID W70797 standard; protein; 592 AA.
AC W70797;
DT 03-FEB-1999 (first entry)
DE Human Interleukin-6R-alpha-Fc.
KW gp130; cytokine antagonist; interleukin; gamma-interferon;
KW granulocyte macrophage colony-stimulating factor; J peptide;
KW transforming growth factor-beta.
OS Synthetic.
OS Homo sapiens.
FH Key
FT Protein
FT Misc_difference 2
FT /label= L2V
FT /note= "changed to accomodate a Kozak sequence"
FT Peptide
FT 1..19
FT /note= "signal peptide"
FT Misc_difference 359..360
FT /note= "Ala-Gly bridge"
FT Protein
FT 361..592
FT /note= "Fc domain of human IgG1"
FT Disulfide_bond 371..374
FT US5844099-A.
PN 01-DEC-1998.
PF 27-NOV-1995; 563105.
PR 27-NOV-1995; US-563105.
PR 20-OCT-1993; US-140222.
PA (REGG-) REGENERON PHARM INC.
PI Economides A, Stahl N, Yancopoulos GD;
DR WPI; 99-044669/04.
PT Cytokine antagonists - comprising extracellular domains of
PT specificity-determining and signal-transducing components of
PT cytokine receptor
PS Example 3; Fig 5; 46pp; English.
CC The present sequence represents the amino acid sequence of human
CC interleukin (IL)-6R-alpha-Fc. The protein is used in the course
CC of the invention. The specification describes cytokine antagonists
CC comprising only the extracellular domain of the specificity-determining
CC component of the cytokine receptor and the extracellular domain of a
CC signal-transducing component of the cytokine receptor. The cytokine
CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
CC granulocyte macrophage colony-stimulating factor (GM-CSF),
CC gamma-interferon or transforming growth factor-beta (TGF-beta). The
CC antagonist is capable of binding the cytokine to form a nonfunctional
CC complex. The compounds have therapeutic activity as cytokine antagonists
CC and can also be used in assays for identifying novel agonists and
CC antagonists of cytokines.
SQ Sequence 592 AA;

Query Match 62.9%; Score 2391; DB 1; Length 592;
Best Local Similarity 99.7%; Pred. No. 5.54e-174;
Matches 322; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MVAVGALLAALLAAPGAALAPRCRPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
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Qy 1 MLAVGALLAALLAAPGAALAPRCRPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
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Db 61 VLKPPAGSHPSRWAGMGRLLRSVQLHDSGNYSYRAGRAGTAVHLLVDVPPPEPQLS 120
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Qy 121 CRRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSOESQKFCQLAV 180
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Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFCGILQDPDPANITVTAVARNPRLSVTWQD 240
|||||
Qy 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFCGILQDPDPANITVTAVARNPRLSVTWQD 240
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Db 241 PHSWNSFFYRLRFELRYRAERSKFTTWMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300
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Qy 241 PHSWNSFFYRLRFELRYRAERSKFTTWMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300
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```


PI Kishimoto T;
DR WPI; 89-264012/37.
DR N-PSDB; P90525.
PT Receptor protein for human B cell stimulating factor-2 - used for
PT developing prophylactic, therapeutic and diagnostic agents for
PT associated disorders.
PS Claim 6; page 39; 76pp; english.
CC The BSF2 receptor has amino acids at the C-terminal deleted. The receptor
CC is derived from a monocytic U937 cell line. It can be used to develop
CC prophylactic and therapeutic pharmaceuticals, as agents to relate
CC diseases and disorders to abnormal BSF-2 prodn. It can also be used to
CC study an immune mechanism with which BSF-2 or the receptor is concerned.
SQ Sequence 323 AA;

Query Match 61.8%; Score 2351; DB 1; Length 323;
Best Local Similarity 98.8%; Pred. No. 7 97e-171;
Matches 318; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1 MLAVGCALLAALLAAGAALAPRRCPADEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
QY 1 MLAVGCALLAALLAAGAALAPRRCPADEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60

Db 61 VLKPKAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
QY 61 VLKPKAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120

Db 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFOEPCQYSOESQKFSQCLAV 180
QY 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFOEPCQYSOESQKFSQCLAV 180

Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTQFGCGILQPDPPANITVTAVARNRWLSVTWQD 240
QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTQFGCGILQPDPPANITVTAVARNRWLSVTWQD 240

Db 241 PHSWNSSYRLRFELRYRAERSKTTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEERFQ 300
QY 241 PHSWNSSYRLRFELRYRAERSKTTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEERFQ 300

Db 301 GGESEWSPAMGTPWTSRSP 322
QY 301 GGESEWSPAMGTPWTSRSP 322

RESULT 13
ID W70805;
AC W70805;
DT 03-FEB-1999 (first entry)
DE Amino acid sequence of the interleukin (IL)-6R-alpha-313 domain.
KW gp130; cytokine antagonist; interleukin; gamma-interferon;
KW granulocyte macrophage colony-stimulating factor; J peptide;
KW transforming growth factor-beta.
OS Synthetic.
FH Key Location/Qualifiers
FT Protein 1..313
FT /note= "truncated interleukin (IL)-6R-alpha domain"

FN US5844099-A.
PD 01-DEC-1998.
PF 27-NOV-1995; 563105.
PR 27-NOV-1995; US-563105.
PR 20-OCT-1993; US-140222.
PA (REGG-) REGENERON PHARM INC.
PI Economides A, Stahl N, Yancopoulos GD;
DR WPI; 99-044669/04.
PT Cytokine antagonists - comprising extracellular domains of
PT specificity-determining and signal-transducing components of
PT cytokine receptor
PS Example 4; Fig 16; 46pp; English.
CC The present sequence represents the amino acid sequence of interleukin
CC (IL)-6R-alpha-313 domain. The protein is used in the course of the
CC invention. The specification describes cytokine antagonists comprising
CC only the extracellular domain of the specificity-determining component of
CC the cytokine receptor and the extracellular domain of a
CC signal-transducing component of the cytokine receptor. The cytokine

is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
granulocyte macrophage colony-stimulating factor (GM-CSF),
gamma-interferon or transforming growth factor-beta (TGF-beta). The
antagonist is capable of binding the cytokine to form a nonfunctional
complex. The compounds have therapeutic activity as cytokine antagonists
and can also be used in assays for identifying novel agonists and
antagonists of cytokines.

Query Match 60.9%; Score 2317; DB 1; Length 315;
Best Local Similarity 99.7%; Pred. No. 3.85e-168;
Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MVAVGCALLAALLAAGAALAPRRCPADEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
QY 1 MVAVGCALLAALLAAGAALAPRRCPADEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60

Db 61 VLKPKAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
QY 61 VLKPKAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120

Db 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFOEPCQYSOESQKFSQCLAV 180
QY 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFOEPCQYSOESQKFSQCLAV 180

Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTQFGCGILQPDPPANITVTAVARNRWLSVTWQD 240
QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTQFGCGILQPDPPANITVTAVARNRWLSVTWQD 240

Db 241 PHSWNSSYRLRFELRYRAERSKTTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEERFQ 300
QY 241 PHSWNSSYRLRFELRYRAERSKTTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEERFQ 300

Db 301 GGESEWSPAMGTP 313
QY 301 GGESEWSPAMGTP 313

RESULT 14
ID R70122 standard; Protein; 1042 AA.
AC R70122;
DT 14-FEB-1996 (first entry)
DE IL8-R type 1-GBP 130 fusion protein.
KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW red blood cell; cytokine receptor; glycoprotein binding peptide 130;
KW GBP 130; GBPH; glycoprotein binding peptide homologue; glycoprotein A.
OS ChimERIC Homo sapiens.
OS ChimERIC Plasmodium falciparum.
FH Key Location/Qualifiers
FT misc_difference 54
FT /label= OTHER
FT /note= "Arn (sic)"

FN WO9506737-A.
PD 09-MAR-1995.
PF 01-SEP-1994; G01900.
PR 03-SEP-1993; GB-018350.
PR 23-AUG-1994; GB-017021.
PA (PREN/) PRENDERGAST K F.
PI Prendergast RF;
DR WPI; 95-115452/15.
PT New hybrid peptide(s) for binding cytokine(s) - comprising a
PT malaria parasite peptide capable of binding a red blood cell and
PT a receptor peptide.
PS Example A; Page 77-78; 93pp; English.
CC Hybrid peptides for binding cytokines, comprising a malaria parasite
CC (Plasmodium falciparum) peptide (capable of binding to a red blood
CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC of these hybrid peptides. R70122 is a fusion of interleukin 6 receptor
CC (as confirmed with reference to SWISSPROT, as it is unclear in the
CC specification whether this sequence is IL6-R or IL8-R type) and
CC glycoprotein binding protein (GBP) 130. The use of cytokine receptors not
CC normally found on RBCs means that the cytokine can bind harmlessly to the
CC RBC without deleterious effect. The RBC protects the hybrid peptides from

CC excretion from the kidney, and due to steric hindrance prevents the
CC cytokines binding to a receptor in another cell. GBP 130 or GBPH
CC (GBP homologue) are the pref. malaria parasite peptides used, others
CC include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA (pre major
CC merozoite surface antigen) and the Duffy binding receptor molecule (eg.
CC exhibited by Plasmodium vivax). These peptides bind to pref. glycophorin
CC A, B and C, sialo glycoproteins, found on the surface of RBCs. The hybrid
CC peptides are thus used to lower the levels of free cytokines in the
CC circulation to reduce pathological damage.
SQ Sequence 1042 AA;

Query Match 55.5%; Score 2110; DB 1; Length 1042;
Best Local Similarity 97.0%; Pred. No. 8.14e-152;
Matches 295; Conservative 0; Mismatches 1; Indels 8; Gaps 2;

Db 1 LAPRCFAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHVLKPKAAGSHPSXWAGMGR 60
QY 20 LAPRCFAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHVLKPKAAGSHPSXWAGMGR 79
Db 61 RLLRSVQLHDSGNYSY-AGRAGTIVHLLVDVPPPEPOLSCFRKSPLSNVVCEWGPGRST 119
QY 80 RLLRSVQLHDSGNYSYRAGRAGTIVHLLVDVPPPEPOLSCFRKSPLSNVVCEWGPGRST 139
Db 120 PSLTTKAVLLVRKFQNSPAEDFQE-----SOKFSQQLAVPEGDSFSFYIVSMCVASSVG 172
QY 140 PSLTTKAVLLVRKFQNSPAEDFQEPCOYSQESQFSQQLAVPEGDSFSFYIVSMCVASSVG 199
Db 173 SKFSKTOTFOGCGTLQDPDPANITVAVARNRWLSVTWODPHSWNSFFYLRLFEYLRYA 232
QY 200 SKFSKTOTFOGCGTLQDPDPANITVAVARNRWLSVTWODPHSWNSFFYLRLFEYLRYA 259
Db 233 ERSKFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPAMGTPWTESR 292
QY 260 ERSKFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPAMGTPWTESR 319
Db 293 SPPA 296
QY 320 SPPA 323

RESULT 15
ID P90526 standard; protein; 386 AA.

AC P90526;
DT 25-JAN-1990 (first entry)
DE B cell stimulating factor-2 receptor.
KW B cell stimulating factor-2 receptor; monocyte U937 cell line.
OS Homo sapiens.
PN AU8928720-A.
PD 27-JUL-1989.
PF 23-JAN-1989; 28720.
PR 22-JAN-1988; JP-012387.
PR 25-JAN-1988; JP-012599.
PR 04-AUG-1988; JP-194885.
PR 14-JAN-1989; JP-007461.
PA (KISH) Tadamoto Kishimoto.
PI Kishimoto T;
DR WPI; 89-264012/37.
DR N-PSDB; P90525.
PT Receptor protein for human B cell stimulating factor-2 - used for
PT developing prophylactic, therapeutic and diagnostic agents for
PT associated disorders.
PS Claim 4; page 37-8; 76pp; english.
CC The BSF2 receptor has residues near the N-terminal deleted. The receptor
CC is derived from a monocyte U937 cell line. It can be used to develop
CC prophylactic and therapeutic pharmaceuticals as agents to relate diseases
CC and disorders to abnormal BSF-2 prodn. It can also be used to study an
CC immune mechanism with which BSF-2 or the receptor is concerned.
SQ Sequence 386 AA;

Query Match 40.3%; Score 1534; DB 1; Length 386;
Best Local Similarity 97.7%; Pred. No. 1.55e-106;
Matches 211; Conservative 0; Mismatches 1; Indels 4; Gaps 2;

Db 28 VDVPPPEPOLSCFRKSPLSNVVVC--GPRSTPEWSLTTKAVLLVRKFQNSPAEDFQEPCOY 85
QY 110 VDVPPPEPOLSCFRKSPLSNVVCEWGPGRSTP--SLTTKAVLLVRKFQNSPAEDFQEPCOY 167
Db 86 SQESQKFSQQLAVPEGDSFSFYIVSMCVASSVGSKFSKTOTFOGCGTLQDPDPANITVAV 145
QY 168 SQESQKFSQQLAVPEGDSFSFYIVSMCVASSVGSKFSKTOTFOGCGTLQDPDPANITVAV 227
Db 146 ARNPRWLSVTWODPHSWNSFFYLRLFEYLRYAERSKFTTMMVKDLQHCVIHDAWSGLR 205
QY 228 ARNPRWLSVTWODPHSWNSFFYLRLFEYLRYAERSKFTTMMVKDLQHCVIHDAWSGLR 287
Db 206 HVVOLRAQEEFGQGEWSEWSPAMGTPWTESRPPA 241
QY 288 HVVOLRAQEEFGQGEWSEWSPAMGTPWTESRPPA 323

Search completed: Thu Aug 10 16:00:00 2000
Job time : 60 secs.

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OM nucleic - nucleic search, using sw model

Run on: August 9, 2000, 05:41:00 ; Search time 1178.81 Seconds
(without alignments)
6030.355 Million cell updates/sec

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Perfect score: 1612
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues
Total number of hits satisfying chosen parameters: 10495684

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	3	364	22.6	481	43	AI751501	AI735329 at09c06.x
C 4	4	297.4	18.4	771	43	AI735329	AI085963 o286h01.x
C 5	5	286.4	17.8	731	35	AI085963	AI242041 wj29h07.x
C 6	6	281	17.4	725	44	AI242041	T29234 EST73852.Hu
C 7	7	248.6	15.4	287	89	T29234	AI472218 tj86e02.x
C 8	8	240.2	14.9	655	40	AI472218	AA381568 EST94686
C 9	9	216.4	13.4	280	25	AA381568	W51812 zc48h04.r1
10	10	210	13.0	618	91	W51812	AA381892 EST95205
11	11	186	11.5	311	25	AA381892	AA380919 EST93950
12	12	172.4	10.7	316	25	AA380919	AI343270 tb94c07.x
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C 14	14	148.2	9.2	311	79	AW630409	AI982185 pat.pk007
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C 17	17	125.6	7.8	463	43	AI751500	AA947476 ok20h06.s
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C 19	19	95.6	5.9	498	28	AA553279	AA721478 nz74g01.s
C 20	20	91.2	5.7	562	30	AA721478	AW214008 uo46e09.x
C 21	21	81	5.0	636	69	AW214008	B87803 RPC111-30H2
C 22	22	79.2	4.9	657	121	B87803	AW519504 up33e08.y
C 23	23	77	4.8	601	73	AW519504	AQ135450 HS_3053_A
C 24	24	76.6	4.8	416	94	AQ135450	AA381453 EST94531
C 25	25	74	4.6	196	25	AA381453	AW637075 b154a09.w
C 26	26	70.2	4.4	617	79	AW637075	AI095255 oy18h07.s
C 27	27	65.8	4.1	493	35	AI095255	AI053013 Drosophila
C 28	28	58.4	3.6	925	122	CNS0091P	AI074123 oz54c06.x
C 29	29	53.2	3.3	473	35	AI074123	AW503691 UI-HF-BN0
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32	32	51.2	3.2	385	72	AW437358	AW243012 xn28c05.x
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C 34	34	50.2	3.1	839	122	CNS004NB	AL101589 Drosophila
C 35	35	49	3.0	645	122	CNS01213	AL066742 Drosophila
C 36	36	47.6	3.0	932	122	CNS0072Q	AL0668051 Drosophila
C 37	37	47.2	2.9	935	122	CNS006XK	AL108460 Drosophila
38	38	47	2.9	1101	123	CNS017SY	AL066742 Drosophila
C 39	39	46.8	2.9	932	122	CNS0072Q	AW134706 UI-H-B11-
C 40	40	46.2	2.9	477	64	AW134706	AW134707 UI-H-B11-
C 41	41	46.2	2.9	477	64	AW134707	T28073 EST26562.Hu
C 42	42	45.6	2.8	361	89	T28073	AA495728 zw04a09.r
C 43	43	44	2.7	446	27	AA495728	AL065629 Drosophila
C 44	44	43.6	2.7	910	122	CNS006ON	AL099352 Drosophila
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ALIGNMENTS

RESULT 1
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DEFINITION hb87a03.y1 NCI-CCGAP-GUI Homo sapiens cDNA clone IMAGE:2969740 5' similar to gb:X04430 INTERLEUKIN-6 PRECURSOR (HUMAN);, mRNA

ACCSSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

sequence.
AW630744
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EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 517)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
On Jan 6, 2000 this sequence version replaced gi:6676648.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CCGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml
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High quality sequence stop: 422.
Location/Qualifiers
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/note="Organ: genitourinary tract; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. primer: Oligo dT. Library constructed by Life Technologies."

FEATURES
source

BASE COUNT
ORIGIN

Query Match
Best Local Similarity
Matches 383; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1042 ccagttacccccagggaagattccaaagattgacgccccacacagacagcactcacc 1101
DB 130 CCAGTACCCCCAGGAGAGATTCCAAAGATGTAGCGCGCCACACAGACAGCCACTCACC 189
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DB 190 TCTTCAGAACGAATTGACAAACAATTCGGTACATCTCTCGACGGCATCTCAGCCCTGAGA 249
QY 1162 aaggagacatgtaacaaagagttaacatgtgtgaaagacagaaagagcactggcagaaaaac 1221
DB 250 AAGGAGACATGTAAACAAAGAGTAACATGTGTGAAGCAGCAAGAGGCGACTGCGCAGAAAAC 309
QY 1222 aaactgaaccttccaaagatgctgtaaaagatgagtgatgcttccaatctgattgtaagatgag 1281
DB 310 AACCTGAACCTTCCAAAGATGCTGAAAAAGATGATGATGCTTCCATCTCGATCAATGAG 369
QY 1282 gagactgtcgtgtaaaatcatcactggtctctttggagtttgaggtatcacctagagtagtac 1341
DB 370 GAGACTGTGCTGTAATAATCATCTGCTCTTTTGGAGTTTGGAGTATACCTAGAGTAC 429
QY 1342 ctccagaacagatttgagagtagtgaggagaaacagcagagctgtgcagatgagtagtaaaa 1401
DB 430 CTCACAGACAGATTTGAGAGTAGTGAGGAACAAGCAGAGCTGTGCGAGTAGTAGTACAAA 489
QY 1402 gtctgatccagtctcctgcgaaaaaagg 1429

Qy	1162	aaggagacatgtacaagagtagtaactgtgtgaagacagcaagagcactgcgcagaaac	121
Db	264	AAGGAGACATGTTAACAGAGTACATGTGTGAAAGCAGCAAGAGAGCACTGGCAGAAAAC	323
Qy	1222	aacctgaacctccaagatggct-gaaaaatcatcac-tggtcttttgagtttgagggtataccctagagt	1280
Db	324	AACCTGAACCTTCCAAGATGGCTGCAAAAGATGGATGCTTCCAATCTGGATTCAATGA	383
Qy	1281	ggagacttgctgtgtaaaatcatcac-tggtcttttgagtttgagggtataccctagagt	1339
Db	384	GGAGACTTGGCTGGTGAATCATCACTTGGCTTTTGAGGTTTTCAGGTATACCTAGAGT	443
Qy	1340	acctccgaacagattgagtag-tgaggaaacagccagagctgtgcagatgagtaca	1398
Db	444	ACCTCCAGAACAGATTGAGTAGTGTGAGGAAACAGCCAGAGCTGTGCAGATGAGTACA	503
Qy	1399	aaagtctgatccagttctctgcagaaaaagcaagaatctagatgcataaacaccccc-	1457
Db	504	AAGTCTGATCCAGTTCCTTGGCAGAAAAAGGCAAGAAATCTAGATGCNATNACCACCCCT	563
Qy	1458	tgacccaaccacaaatgccagcctgctgcaga	1489
Db	564	TGACCCCAACCAATGCCAGCTGCTGACGA	595
RESULT 3			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			
Query Match			
Best Local Similarity			
Matches			
Query Match			
Best Local Similarity			
Matches			
Query Match			
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Best Local Similarity			
Matches			

```
QY 1042 ccagtacccccagagagattccaaagatgtagcccccacacacagacagccactcacc 1101
|||||
Db 118 CCAGTACCCCGAGAGAGATTCCAAGATGTACCGCCGCCACACACAGACCCACTCACC 177
|||||
QY 1102 tcttcagaagaattgacaacaattcgggtacatctctcagcgcatctcagccctgaga 1161
|||||
Db 178 TCTTCAGAACGAATTGACAAACAAATTCGGTACATCTCTCGACGGCATCTCAGCCCTCAGA 237
|||||
QY 1162 aagagacatgttaacaagagtaacatgtgaaagcagcaaaagagcactggcagaaaaac 1221
|||||
Db 238 AAGGAGACATGTAAACAAGAGTAACATGTGTAAAGCAGCAAAAGAGGCACTGGCAGAAAAC 297
|||||
QY 1222 aacctgaacctctcaaaagatggtgaaagagatgattgcttcccaatctggtattcaatgag 1281
|||||
Db 298 AACTGTGAACCTTCCAAGATGGCTGAAAGAGATGATGCTTCCAATCTGGATTCAATGAG 357
|||||
QY 1282 gagacttgcttggtgaaatactcactggtcttcttggagtttgaggtatatacctagatgac 1341
|||||
Db 358 GAGACTTGCTGTGTGAAATCATCACTGGTCTTTTGGAGTTTGAGGTATACCTAGAGTAC 417
|||||
QY 1342 ctccagacagattgagtagtgaggaacaagcagagactgtgcagatgagtacaaaa 1401
|||||
Db 418 CTCAGAACAGATTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAAA 477
|||||
QY 1402 gtcc 1405
|||||
Db 478 GTCC 481
|||||

RESULT 4
AI735329/c
LOCUS AI735329 771 bp mRNA EST 14-JUN-1999
DEFINITION at09c06.xl Barstead aorta HPLRB6 Homo sapiens cDNA clone
IMAGE:2354602 3' similar to gb:X04430 INTERLEUKIN-6 PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION AI735329
VERSION AI735329.1 GI:5056853
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 771)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Contact: Wilson RK
Unpublished (1997)
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from Gbco
High quality sequence stop: 432.
LOCATION/Qualifiers
1. .771
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2354602"
/clone_lib="Barstead aorta HPLRB6"
/sex="male"
/dev_stage="adult, age 64"
/lab_host="DH10B (phage resistant)"
/note="Organ: aorta; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st
strand cDNA was primed with a Not I - oligo(df) primer [5'
TGTTAGCAATCTCAAGTGGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTTTTTT
```

```
3'); double-stranded cDNA was ligated to Eco RI adaptors
[5' AATTGGATCGAAC 3' and 5' GTTGGATCGG 3'], digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library constructed by Bob
Barstead."
BASE COUNT 240 a 156 c 128 g 241 t 6 others
ORIGIN
Query Match 18.4%; Score 297.4; DB 43; Length 771;
Best Local Similarity 90.1%; Pred. No. 2.3e-68;
Matches 327; Conservative 0; Mismatches 35; Indels 1; Gaps 1;
QY 1249 aaagatgagtgcttcccaatctggattccaatgagagacttgcctggtgaaatcatcact 1308
|||||
Db 771 AAAAGGTGAATGCTCCATCTTGATCAATGAGGAGACTTGCCTGGTGAANATCATCATG 712
|||||
QY 1309 ggtctttggagttgaggtatacctagagtacctccagaacagatttgagtagtagag 1368
|||||
Db 711 GTCTTTTGTAGTTGAGGGTATACCTTAGAGTACCTCCAGAACAGATTGAGAGTAGTAG 652
|||||
QY 1369 gaacaagccagagctgtccagatgagtacaaaagtcctgacatccagttcctcagaaaaag 1428
|||||
Db 651 GAACAAGCAAGAGCTGTGCAGATGAGTACANAAGTCTCTGATCCAGTTCTNTGCAGAAAAG 592
|||||
QY 1429 gcaagaatctagatgcaataaccaccctgaccccaaccacaatgccagctgctgacg 1488
|||||
Db 591 G-AAAGAATCTAGATGCAATAACCCCTGACCCGACCAAAATGCCAGCCTGCTGAGC 533
|||||
QY 1489 aagctgcaggcacagaaccagtgctgcaggacatgacaaactcatctcttcgcgagc 1548
|||||
Db 532 AAGTGCAGGCACAGAACCCAGTGGCTGCAGGACATGACAACTCATCTCTGCGCAGC 473
|||||
QY 1549 tttaagagttcttcgactccagctcagctgaggtcttcggcaaatgacatgggcacogt 1608
|||||
Db 472 TTTAAGGAGTCTCTGCAGTCCAGCTGAGGTTCTTTCGGCAAAATGTAGCATGGGCACCTC 413
|||||
QY 1609 cga 1611
|||||
Db 412 AGA 410
|||||

RESULT 5
AI085963/c
LOCUS AI085963 731 bp mRNA EST 17-AUG-1998
DEFINITION o286h01.xl Soares senescent fibroblasts NBHSF Homo sapiens CDNA
clone IMAGE:1682257 3' similar to gb:X04430 INTERLEUKIN-6 PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION AI085963
VERSION AI085963.1 GI:3424386
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 731)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Apr 7, 1998 this sequence version replaced gi:3036013.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 445.
LOCATION/Qualifiers
1. .731
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1682257"
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```

/clone_lib="Soares_senescent_fibroblasts_NbHSF"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/notes="Vector: pT7T3D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5',
TGTATCAACATCTCAAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo."
233 a 143 c 123 g 231 t 1 others
BASE COUNT
ORIGIN

```

Query Match	17.8%;	Score 286.4;	DB 35;	Length 731;
Best Local Similarity	94.5%;	Pred. No. 1.9e-65;		
Matches 307;	Conservative 0;	Mismatches 17;	Indels 1;	Gaps 1;
QY 1288	tgccctgataaaatcatcactggtctctttggagatttgaaggtataacctagatcacctccag	1347		
Db 731	TCGCTGGTTGAAATCATCACGTGCTCTTTGGAGTTTGAGGTATACTAGAACTACTTCAAG	672		
QY 1348	aacgatttgagatgtaggagaacagccagagctgtgcagatgagtcacaaaagtcc-t	1406		
Db 671	ACCAGATTGAGACTAGTGAGGAACAAGCCAAAGCTGTGCAGATGAGTACAAAAGTCCTT	612		
QY 1407	gaccagtctctgcagaaaaaggcaagaatctatagatgcaataaccacccctgaccacaac	1466		
Db 611	GATCCAGTCTTTCGAGAAAAAGGCAAGAAATCTAGATGCAATAACACCCCTGACCCAAC	552		
QY 1467	cacaaatgcagcctgctgacgaagctgcaggcacagaaaccagttggctgcaggacatgac	1526		
Db 551	CACAAATGCCAGCCTGCTGAGGAAGCTGCAGGCACAGAACCCAGTGGCTGCGAGGACATGAC	492		
QY 1527	aactcaatctattctgcgcagctttaaggagttcctgcagtcacagcctgaggggtctcttcg	1586		
Db 491	AACTCATCTATTCTGGCGACGTTTAAGGAGTTCCTGCAGTCCAGCCTGAGGGGCTCTCG	432		
QY 1587	gcaaatgtagcatggggcacccgtcga	1611		
Db 431	GCAAAATGTAGCATGGGCACCTCAGA	407		

RESULT 6
AI824041/c
LOCUS
DEFINITION w129107.x1 NCI_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2404285 3', similar to gb:X04430 INTERLEUKIN-6 PRECURSOR (HUMAN);, mRNA
sequence.
VERSION AI824041
KEYWORDS AI824041.1 GI:5444712
SOURCE EST.
ORGANISM human.
REFERENCE Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 725)
NCI-Cgap <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center

```

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1194   Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 450.
      Location/Qualifiers
1. .725
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /clone="IMAGE:2404285"
   /clone_lib="NCI_CGAP_Kid12"
   /tissue_type="2 pooled tumors (clear cell type)"
   /lab_host="DH108"
   /note="Organ: kidney; Vector: p7T73D-Pac (Pharmacla) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid5 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1323912-1325831, 1471368-1472903 and
1492104-1493255). Subtraction by Bento Soares and M.
Fatima Bonaldo. "
232 a 142 c 125 g 226 t
BASE COUNT
      ORIGIN

```

[illegible]

RESULT	7
LOCUS	T29234
DEFINITION	ESTF73852 Human Bone Homo sapiens cDNA 5' end similar to interleukin 6 (HT:1314), mRNA sequence.
ACCESSION	T29234
VERSION	T29234.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,

Clayton, R.A., Cline, R.T., Cotton, M.D., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodde, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S., Kelley, J.M., Kline, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Hasetline, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Million Basepairs of cDNA Sequence

Nature 377, 3-174 (1995)

JOURNAL
MEDLINE
COMMENT

On Dec 20, 1995 this sequence version replaced gi:1135864.
 Contact: Venter, JC
 The Institute for Genomic Research
 932 Clopper Rd, Gaithersburg, MD 20878
 Tel: 3018699056
 Fax: 3018699423

Email: tdbinfo@tdb.tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please contact the TIGR Database
 (tdbinfo@tdb.tigr.org)

Insert Length: 716 Std Error: 0.00

Seq primer: M13 Reverse

High quality sequence stop: 92.

Location/Qualifiers

1..287

/organism="Homo sapiens"

/db_xref="Arcc (inhost):105671"

/db_xref="taxon:9606"

/clone_lib="Human Bone"

/tissue_type="bone"

81 a 69 c 65 t 4 others

BASE COUNT 81 a 69 c 65 t 4 others

ORIGIN

Query Match 15.4%; Score 248.6; DB 89; Length 287;
 Best Local Similarity 96.9%; Pred. No. 1.6e-55;
 Matches 251; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1353 atttgagtagttaggaacaagccagagctgtgcagatgagtaacaaagtcttgatcca 1412

Db 1 ATTTGAGTAGTGCAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAANTCCTGATCCA 60

QY 1413 gtctctcagaaaagcaagaatctagatgcaataaccacccctgacccaaccacaaa 1472

Db 61 NTTCTGCAGNAAAGGCAGAGANTCTAGATGCATATACACCCCTGACCCACCAACA 120

QY 1473 tgccagcctgtgcagagctgcaggcacagaaccagtggtgcagagatgacaaactca 1532

Db 121 TGCCAGCNTGCTGCAGAGCTGCAGGCACAGAACCACTGCTGCAGGACATGACAACTCA 180

QY 1533 tctaatctcgcagagctttaagagattctctgcagctcagagctgagggctcttcggcaaat 1592

Db 181 TCTCATTTCTCGCAGTGTAAAGGAGTTCTGCAGTCCAGCTGAGGGCTCTTCGGCAAAAT 240

QY 1593 gtacatgggacccgtcga 1611

Db 241 GTAGCATGGGCACCTCAGA 259

RESULT 8

AI472218/c

LOCUS

DEFINITION tJ86e02.x1 Soares.NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone

IMAGE:2148410.3 similar to gb:X04430 INTERLEUKIN-6 PRECURSOR

(HUMAN); mRNA sequence.

AI472218 655 bp mRNA EST 14-APR-1999

EST

tJ86e02.x1 Soares.NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone

IMAGE:2148410.3 similar to gb:X04430 INTERLEUKIN-6 PRECURSOR

(HUMAN); mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AI472218

AI472218.1

GI:4334308

human

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 655)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

On May 18, 1998 this sequence version replaced gi:3138589.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 709 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 444.

Location/Qualifiers

1..655

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Soares.NSF_F8_9W_OT_PA_P_S1"

/lab_host="DH10B"

/note="Organ: pooled; Vector: pTT73D-Pac (Pharmacia) with

a modified polylinker; Site_1: Not 1; Site_2: Eco RI;

Equal amounts of plasmid DNA from five normalized

libraries were mixed, and ss circles were made in vitro.

Following HAP purification, this DNA was used as tracer in

a subtractive hybridization reaction. The driver was

PCR-amplified cDNAs from pools of 5,000 clones made from

the same 5 libraries. The pools consisted of the following

libraries and cloneIDs: Soares NBHSF pool 1:

309384-310919, 323208-325895 Soares Nb2HP pool 1:

145032-147335, 147720-148103, 148872-149255, 15002 -

150407, 151176-152327 Soares Nb2HF8-9W pool 1:

758280-760583, 772104-774407 Soares NBHPA pool 1:

304776-306311, 320136-322823, 326280-326663 Soares NBHOT

pool 1: 723720-726407, 739080-740999 Subtraction by Bento

Soares and M. Fatima Bonaudo."

BASE COUNT 201 a 125 c 113 g 213 t 3 others

ORIGIN

Query Match 14.9%; Score 240.2; DB 40; Length 655;
 Best Local Similarity 97.6%; Pred. No. 3.4e-53;
 Matches 242; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1364 gtgaggacaagccagagctgtgcagatgagtaacaaagtctcattccagttcttgaga 1423

Db 655 GTGAGGCAACAGCCAGAGCTGTGCAGATGAGTACAAAGTCNTGATCCAGTCTCTGCAGA 596

QY 1424 aaaaggcaagaatctagatgcaataaccacctgacccaaccacacaaatccagctgc 1483

Db 595 AAAAGGCAAGAATCTAGATGCAATTAACCCCTGACCCCAACCAACNATGCCAGCTGC 536

QY 1484 tgacgaagctgcaggcacagaaccagtggtgcaggagatgacaaactcattcttcgc 1543

Db 535 TGACGAAGCTGCAGCACAGAACCCAGTGGCTGCAGGACATGACAACTCATCTCATTTCTGC 476

QY 1544 gcagcttaaggagttctctcagtcagtcagctcagggctcttcgcgaatgtagcatgggc 1603

Db 475 GCAGCTTTAAGGAGTCTCTGCAGTCCAGCTTGAGGGCTCTTCGGCAAAATGTAGCATGGGC 416

QY 1604 accgtcga 1611

Db 415 ACCTCAGA 408

Db 183 CTGGCCCTGGTGAATAATCACTACCTGGTCTTTTGGAGTTGAGGTATACCTAGAGTACCTCC 242

QY 1346 agacagattgagtagtagtgaggaaacagcagact 1383 11-OCT-1996

Db 243 AGAAGAGATTGAGTAGTACTGAGGAACAGCCAGAGCT 280

RESULT 10

W51812 618 bp mrna EST 11-OCT-1996

LOCUS zc48h04.r1 Soares senescent fibroblasts_NbHSF Homo sapiens cDNA

DEFINITION clone IMAGE:375591.5' similar to gb.X04430 INTERLEUKIN-6 PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION W51812 GI:1349685

VERSION W51812.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 618)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilsson, K.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT On Apr 7, 1998 this sequence version replaced gi:3036007. Contact: Willson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 733 Std Error: 0.00

Seq primer: EPrimer

High quality sequence stop: 493.

Location/Qualifiers

1. .618

/organism="Homo sapiens"

/db_xref="GDB:1257103"

/db_xref="taxon:9606"

/clone="IMAGE:325591"

/clone_lib="Soares senescent_fibroblasts_NbHSF"

/tissue_type="senescent fibroblast"

/lab_host="DH10B (ampicillin resistant)"

/note="Vector: p773D (Pharmacia) with a modified polylinker V-YPE; phagemid; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3']

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 185 a 109 c 121 g 192 t 11 others

ORIGIN

Query Match 13.0%; Score 210; DB 91; Length 618;

Best Local Similarity 96.8%; Pred. No. 3.5e-45;

Matches 213; Conservative 0; Mismatches 7; Indels 0; Gaps 0

QY 1392 gattacaaagtctgattcagttctgcagaaaaagcaagaatctagatgcaataac 1451

Db 13 GGTGACAAAGTCTGATCAGTTCCTGCAGAAAAGGCAAGAATCTAGATGCAATGAC 72


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QY 1452 caccctgaccacacaaatgcagcctgctgacgaagtgcaggcacagacacagtg 1511
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Db 73 CACCCTTGACCAACCAACAAATGCCAGCCTGCTGACGAAGCTGCAGGCACAGAACCAAGT 132

QY 1512 gctgcaggacatgacaaactcatctcattctgcgcagctttaagaggttcttcgagtcag 1571
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Db 133 GCTGCAGGACATGACAACTCATCTCATCTCTGCGCANTTTAAAGGAGTTCCTGCAGTCCAG 192

QY 1572 cctgcaggctcttcgcaaatgacatggccaccgctcga 1611
      |||||||
Db 193 CTTGAGGCGCTCTTCGGCAATGTAGCATGGGCACCTCAGA 232

RESULT 11
AA381892
LOCUS
DEFINITION
  AA381892 311 bp mRNA EST 21-APR-1997
  EST95205 Activated T-cells 1 Homo sapiens cDNA 5' end similar to
  Interleukin 6, mRNA sequence.
ACCESSION
  AA381892
VERSION
  AA381892.1 GI:2034376
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 311)
AUTHORS
  Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
  Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
  White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
  Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
  Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
  Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
  Kelley,J.M., Kelley,J.F., McDonald,L.A., Marmaros,S.M., Merrick,J.M.,
  Moreno-Palauques,R.F., Nguyen,D.T., Pelligrino,S.M.,
  Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
  Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
  Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
  Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
  He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
  Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
  Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
  Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
  Fraser,C.M. and Venter,J.C.
  Initial assessment of human gene diversity and expression patterns
  based upon 83 million nucleotides of cDNA sequence
  Nature 377 (6547 Suppl), 3-174 (1995)
12140200
Other_ESTs: THC167228
Contact: Kerlavage, AR
Bioinformatics
  The Institute for Genomic Research
  9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlavet@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
  Location/Qualifiers
    1. .311
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BASE COUNT 86 a 99 c 68 g 58 t
ORIGIN

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Query Match 11.5%; Score 186; DB 25; Length 311;
Best Local Similarity 100.0%; Pred. No. 6.8e-39;
Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1042 ccagtacccccagagagattccaaagatgtgcccgcacacagacagccactcacc 1101
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Db 126 CCAGTAGCCCCAGAGAGAGATTCCAAAGATGTAGCCGCCGCCACACAGACGCCACTCACC 185

QY 1102 tcttcagaacgaattgacaaacaaattcgttacatctcctcagcgcatctcagccctaga 1161
      |||||||
Db 186 TCTTCAGAACGAATTGACAAACAAATTCGGTACATCTCGACGGCATCTCAGCCCTGAGA 245

QY 1162 aaggagacatgtaacaagagtagtaacatgtgtgaagcagcagaagagcactgcgagaaaac 1221
      |||||||
Db 246 AAGGAGACATGTACAAGAGTAGTAACATGTGTGAAGACGACGAAGGCACTGGCAGAAAAC 305

QY 1222 aacctg 1227
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Db 306 AACCTG 311

RESULT 12
AA380919
LOCUS
DEFINITION
  AA380919 316 bp mRNA EST 21-APR-1997
  EST93950 Activated T-cells V Homo sapiens cDNA 5' end similar to
  Interleukin 6, mRNA sequence.
ACCESSION
  AA380919
VERSION
  AA380919.1 GI:2033259
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 316)
AUTHORS
  Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
  Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
  White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
  Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
  Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
  Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
  Kelley,J.M., Kelley,J.F., McDonald,L.A., Marmaros,S.M., Merrick,J.M.,
  Moreno-Palauques,R.F., Nguyen,D.T., Pelligrino,S.M.,
  Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
  Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
  Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
  Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
  He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
  Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
  Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
  Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
  Fraser,C.M. and Venter,J.C.
  Initial assessment of human gene diversity and expression patterns
  based upon 83 million nucleotides of cDNA sequence
  Nature 377 (6547 Suppl), 3-174 (1995)
12140200
Other_ESTs: THC167228
Contact: Kerlavage, AR
Bioinformatics
  The Institute for Genomic Research
  9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlavet@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
  Location/Qualifiers
    1. .316
      /organism="Homo sapiens"
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FEATURES
  source

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from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351).

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Best Local Similarity 96.4%; Pred. No. 7.4e-29;
Matches 161; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1042 ccagtacccccagagagattccaaagatgtatgagcccccacacagagccactcacc 1101
Db 138 CCAGTACCCCCAGAGAGATTCAAAGATGTAGCCGCCCCACACAGACGACCCACTCACC 197
QY 1102 tcttcagaagaaattgacaacaaattcgtacatctcgcagcgcacatcagccctgaga 1161
Db 198 TCTTCAGAACGAATTGACAAACATNTCGGTACGTCTCTGACGGCATCTCAGCCCTGAGA 257
QY 1162 aaggagacatgtaacaaagagtaaca-tgtgtgaagcagcaaaaggg 1207
Db 258 AAGGAGACATGTAACANGAGTAGCATTTGTGTGAAGACGACGAAGAGG 304

RESULT 15
AI982185 628 bp mRNA EST 15-SEP-1999
LOCUS pat.pk0076.f2.f chicken activated T cell cDNA Gallus gallus cDNA
DEFINITION clone pat.pk0076.f2.f 5' similar to interleukin-6, mRNA sequence.
ACCESSION AI982185
VERSION AI982185.1 GI:5885213
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 628)
Tirunagaru.V.G., Sofer,L. and Burnside,J.
AUTHORS An expressed-sequence-tag database of activated chicken T cells:
TITLE sequence analysis of 5596 clones
JOURNAL Unpublished (1999)
COMMENT On Jun 22, 1998 this sequence version replaced gi:3247580.
Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-1345
Fax: 302 831-3651
Email: joan@udel.edu
Seq primer: T7.
FEATURES
source Location/Qualifiers
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/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="pat.pk0076.f2.f"
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/clone_lib="chicken activated T cell cDNA"
/sex="male"
/cell_type="Con A-activated splenic T cell"
/lab_host="E.coli TOP10 F"
/note="Vector: pCDNA3"
BASE COUNT 152 a 170 c 177 g 128 t 1 others
ORIGIN

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Best Local Similarity 56.1%; Pred. No. 2.5e-26;
Matches 262; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 1129 cgggtacatctcagcgcatctcagccctgagaagagagacatgtaacagagtaacatg 1188
Db 45 CGGTGCTGCGGACCGCGCGCGTCCAGCTGCAGGACGAGATGTCAAGAGTTCACCGTG 104
QY 1189 tgtgaagcagcaagagagcactggcagcaaaacacaccttccaaagatggctgaa 1248
Db 105 TGGGAGAACAGCATGGAGATGCTCGTCCGGACAAACCTCAACCTGCCCAAGGTGACGGAG 164
QY 1249 aagatggatgcttccaatgattcaatgagagagacttgcctggtgaaatcatcact 1308

Db 165 GAGGACGGCTGCCTGCTCGCGGGCTTCGACGAGGAGAAATGCCTGACGAACTCTCCAGC 224
QY 1309 ggtcttttgaggtttgaggtatacctagtagtacctccagacagatttgagagtagtgag 1368
Db 225 GGCCTGTTGCGCTTTCAGACCTACCTGGAATTCAATTCAGAGACTTTTCGATAGGGAAG 284
QY 1369 gaacaagccagagctgtgcagatgagtacaaaagtcctgatccagttcctgcagaaaaag 1428
Db 285 CAGAACGTCGAGTCTCTGTGCTACAGCACAAAGCACCTGGCGGCCACGATCCGGCAGATG 344
QY 1429 gcaagaatctagatgcaataaccacccctgaccccaaccacaaatgcagcctgctgacg 1488
Db 345 GTGATAAATCCGATGAAGTGTGTCATCCGACACTCGGCGGCCAGAAATCCTCTCTGCC 404
QY 1489 aagctcagggcacagaaacccagtgctgcagagacatgacaactcatctcttcgcagc 1548
Db 405 AATCTGAAGTCAGATAAGGACTGGATAGAGAAATACCATGACCTCATCTCTCCGAGAC 464
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Db 465 TTTACTTCGTTTATGGAGAAAGACCGTGAGGGCCGCTTCGCTATTGAA 511

Search completed: August 9, 2000, 05:41:10
Job time: 61707 sec

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	995	61.7	2061	7	5171840-1	Patent No. 5171840
2	995	61.7	2061	7	5480796-1	Patent No. 5480796
3	969	60.1	1074	3	US-08-627-151A-15	Sequence 15, Appl
4	969	60.1	1404	7	5171840-8	Patent No. 5171840
5	969	60.1	1404	7	5480796-8	Patent No. 5480796
6	563.6	35.0	1145	7	5510472-1	Patent No. 5510472
7	551.8	34.2	555	1	US-08-437-680A-1	Sequence 1, Appl
8	550.4	34.1	561	1	US-07-745-382-19	Sequence 19, Appl
9	550.4	34.1	561	1	US-07-921-848-19	Sequence 19, Appl
10	550.4	34.1	561	1	US-08-165-301A-19	Sequence 19, Appl
11	550.4	34.1	561	6	PCR-US94-14179-19	Sequence 19, Appl
12	538.6	33.4	951	6	US-08-469-318-57	Sequence 57, Appl
13	538.6	33.4	951	6	PCR-US95-01185-57	Sequence 57, Appl
14	538.4	33.4	540	6	PCR-US94-12873-3	Sequence 3, Appl
15	535.8	33.2	555	2	US-08-567-047-1	Sequence 1, Appl
16	535.8	33.2	555	3	US-08-567-048-1	Sequence 1, Appl
17	531.2	33.0	561	5	US-08-469-318-175	Sequence 175, App
18	531.2	33.0	561	6	PCR-US95-01185-175	Sequence 175, App
19	529.4	32.8	555	3	US-08-693-182-1	Sequence 1, Appl
20	529.4	32.8	555	4	US-09-008-482-1	Sequence 1, Appl
21	526.2	32.6	555	4	US-08-945-529-1	Sequence 4, Appl
22	526.2	32.6	555	4	US-08-945-529-4	Sequence 4, Appl
23	526.2	32.6	555	4	US-08-945-529-5	Sequence 5, Appl
24	526.2	32.6	555	4	US-08-945-529-6	Sequence 6, Appl
25	525	32.6	525	1	US-08-009-973-2	Sequence 2, Appl
26	491	30.5	555	4	US-08-945-529-7	Sequence 7, Appl

Db 641 gtgagtggtgctcctcagagcaccaccatccctgcagcagcaaaagctgtgctcttggtgagga 700
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Db 701 agtttcagaaacagtcctcggccgaagacttccagagcgtgacagctattccagagtcctc 760
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Qy 908 tctgccccag 967
Db 1121 tctgccccag 1180
Qy 968 gcagccttgag 1002
Db 1181 gcagccttgag 1215

RESULT 2
5480796-1
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO: 1:
; LENGTH: 2061
5480796-1

Query Match 61.7%; Score 995; DB 7; Length 2061;
Best Local Similarity 100.0%; Pred. No. 2.8e-247;
Matches 995; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 221 catgagtggtgtagccgag 280
Qy 68 tctgccccagc 127
Db 281 tctgccccagc 340
Qy 128 gaggcgtgctgacagctcctcag 187
Db 341 gaggcgtgctgacagctcctcag 400

Qy 188 cggagagaaatgccactgttcaactgggtgctcaggaagccggctgcaggtcccccacccca 247
Db 401 cggagagaaatgccactgttcaactgggtgctcaggaagccggctgcaggtcccccacccca 460
Qy 248 gcagatgggctggcatgggaaggaggtgctgctgaggtgcgtgcagctccacagactctg 307
Db 461 gcagatgggctggcatgggaaggaggtgctgctgaggtgcgtgcagctccacagactctg 520
Qy 308 gaaactattcatgctacccggccggccggccggccggccggccggccggccggccggccggccgg 367
Db 521 gaaactattcatgctacccggccggccggccggccggccggccggccggccggccggccggccgg 580
Qy 368 ttccccccggagagcagcagctctcctgcttccggaagagcccccctcagcaatttttt 427
Db 581 ttccccccggagagcagcagctctcctgcttccggaagagcccccctcagcaatttttt 640
Qy 428 gtgagtggttctcctcggagcaccaccatccctgcagcagcaaaaggctgtctcttggtagga 487
Db 641 gtgagtggttctcctcggagcaccaccatccctgcagcagcaaaaggctgtctcttggtagga 700
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Db 701 agtttcagaaacagtcctcggccgaagacttccagagcgtgacagctattccagagtcctc 760
Qy 548 agaagttctcctcggcagtagcagtcctcggagagagagagagagagagagagagagagagagag 607
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Db 941 gctggtcagtgtagcagtcctcggag 1000
Qy 788 ggttgagtcagatcgggctgagcgtgcaagcgttcaagacattcacaacatgagtgcaag 847
Db 1001 ggttgagtcagatcgggctgagcgtgcaagcgttcaagacattcacaacatgagtgcaag 1060
Qy 848 acctccagcatcactgtgctacacagcagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagc 907
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Qy 908 tctgccccag 967
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Qy 968 gcagccttgag 1002
Db 1181 gcagccttgag 1215

RESULT 3
US-08-627-151A-15
; Sequence 15, Application US/08627151A
; Patent No. 5866341
; GENERAL INFORMATION:
; APPLICANT: SPINELLA, Dominic
; APPLICANT: BECHERER, Kathleen
; APPLICANT: BROWN, Steven
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: SCREENING DRUG LIBRARIES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 10210 Genetic Center Drive
; CITY: San Diego
; STATE: CA

QY 394 tgcctccggaagagccccctcagcaatgtttgtgagtggttccctcgagcaccoca 453
Db 361 tgcctccggaagagccccctcagcaatgtttgtgagtggttccctcgagcaccoca 420
QY 454 tccctcagcagcaaaagcgtgctctgtgtgaggaatttcagaaacagtcgcgcgcgaagac 513
Db 421 tccctcagcagcaaaagcgtgctctgtgtgaggaatttcagaaacagtcgcgcgcgaagac 480
QY 514 tccagggagcgcgtgcagattccacagagtcaccagaatttcctcgcagttacagtc 573
Db 481 tccagggagcgcgtgcagattccacagagtcaccagaatttcctcgcagttacagtc 540
QY 574 ccggaggagacagctctttctacatagttccatgtcgtgcgcgcagtagtgcgcggagc 633
Db 541 ccggaggagacagctctttctacatagttccatgtcgtgcgcgcagtagtgcgcggagc 600
QY 634 aagttcagcaaaactcaaaccttttcaggggtgtggaattctgcagcctgataccgcctgcc 693
Db 601 aagttcagcaaaactcaaaccttttcaggggtgtggaattctgcagcctgataccgcctgcc 660
QY 694 aacatcacagtcacgtccgtgcgcagaaacccccgcgtgcgtcagtgctacacgtgcaagac 753
Db 661 aacatcacagtcacgtccgtgcgcagaaacccccgcgtgcgtcagtgctacacgtgcaagac 720
QY 754 cccactcctggaactcatctttctacagactacggtttgtgagtcagatatcgggctgaa 813
Db 721 cccactcctggaactcatctttctacagactacggtttgtgagtcagatatcgggctgaa 780
QY 814 cggctcaagacattcaaacatggtgtgcaaggacctccagcactcagtcagtcacac 873
Db 781 cggctcaagacattcaaacatggtgtgcaaggacctccagcactcagtcagtcacac 840
QY 874 gacgcctgagcgcgtgagcagcagtggtcagcttcgtcccagagagatttcgggcaa 933
Db 841 gacgcctgagcgcgtgagcagcagtggtcagcttcgtcccagagagatttcgggcaa 900
QY 934 ggcgagtgagcgcgtgagcagcagtggtcagcttcgtcccagagagatttcgggcaa 993
Db 901 ggcgagtgagcgcgtgagcagcagtggtcagcttcgtcccagagagatttcgggcaa 960
QY 994 cctccagct 1002
Db 961 cctccagct 969

RESULT 5
5480796-8
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:8:
; LENGTH: 1404
5480796-8

Query Match 60.18; Score 969; DB 7; Length 1404;
Best Local Similarity 100.0%; Pred. NO. 1.2e-240;
Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 34 atgctggcgcgtcgcgtgcgcgtgcgcgtgcgcgtgcgcgtgcgcgtgcgcgtgcgcgtg 93
Db 1 atgctggcgcgtcgcgtgcgcgtgcgcgtgcgcgtgcgcgtgcgcgtgcgcgtgcgcgtg 60
QY 94 gcccccaggcgtccctcgcgcagagtggtgcaagagcgtgctgacacagtcgtccagga 153

Db 61 gcccccaggcgtccctcgcgcagagtggtgcaagagcgtgctgacacgtctgcagga 120
QY 154 gacagcgtgactcgtgacctgcccggtgagccggaagacaaatgcacgttctcaactgg 213
Db 121 gacagcgtgactcgtgacctgcccggtgagccggaagacaaatgcacgttctcaactgg 180
QY 214 gtgctcaggaagcgcgtgcaggtcccccagcagatgggtgcgcagtggaagaggg 273
Db 181 gtgctcaggaagcgcgtgcaggtcccccagcagatgggtgcgcagtggaagaggg 240
QY 274 ctgctgctgaggtgcgtgcagctccacgactctggaactattcatctacccggtccggtc 333
Db 241 ctgctgctgaggtgcgtgcagctccacgactctggaactattcatctacccggtccggtc 300
QY 334 cgcacagtggtgagctgtgcaactgtggtggtggttccccccgagagagccacgtctcc 393
Db 301 cgcacagtggtgagctgtgcaactgtggtggtggttccccccgagagagccacgtctcc 360
QY 394 tgcctccggaagagccccctcagcaatgtttgtgagtggttccctcgagcaccoca 453
Db 361 tgcctccggaagagccccctcagcaatgtttgtgagtggttccctcgagcaccoca 420
QY 454 tccctcagcagcaaaagcgtgctcttgcgtgaggaatttcagaaacagtcgcgcgcgaagac 513
Db 421 tccctcagcagcaaaagcgtgctcttgcgtgaggaatttcagaaacagtcgcgcgcgaagac 480
QY 514 tccagagcgcgtgccagattccacagagtcaccagaatttcctcgcagttacagtc 573
Db 481 tccagagcgcgtgccagattccacagagtcaccagaatttcctcgcagttacagtc 540
QY 574 ccggaggagacagctctttctacatagttccatgtcgtgcgcgcagtagtgcgcggagc 633
Db 541 ccggaggagacagctctttctacatagttccatgtcgtgcgcgcagtagtgcgcggagc 600
QY 634 aagttcagcaaaactcaaacctttcaggggtgtggaattctgcagcctgataccgcctgcc 693
Db 601 aagttcagcaaaactcaaacctttcaggggtgtggaattctgcagcctgataccgcctgcc 660
QY 694 aacatcacagtcacgtccgtgcgcagaaacccccgcgtgcgtcagtcagtcacacgtgcaagac 753
Db 661 aacatcacagtcacgtccgtgcgcagaaacccccgcgtgcgtcagtcagtcacacgtgcaagac 720
QY 754 cccactcctggaactcatctttctacagactacggtttgtggaattctgcagcctgataccgcctgcc 813
Db 721 cccactcctggaactcatctttctacagactacggtttgtggaattctgcagcctgataccgcctgcc 780
QY 814 cggctcaagacattcaaacatggtgtgcaaggacctccagcactcagtcagtcacac 873
Db 781 cggctcaagacattcaaacatggtgtgcaaggacctccagcactcagtcagtcacac 840
QY 874 gacgcctgagcgcgtgagcagcagtggtcagcttcgtcccagagagatttcgggcaa 933
Db 841 gacgcctgagcgcgtgagcagcagtggtcagcttcgtcccagagagatttcgggcaa 900
QY 934 ggcgagtgagcgcgtgagcagcagtggtcagcttcgtcccagagagatttcgggcaa 993
Db 901 ggcgagtgagcgcgtgagcagcagtggtcagcttcgtcccagagagatttcgggcaa 960
QY 994 cctccagct 1002
Db 961 cctccagct 969

RESULT 6
5510472-1
; Patent No. 5510472
; APPLICANT: REVEL, MICHEL, TIOLLAIS, PIERRE
; TITLE OF INVENTION: PRODUCTION OF RECOMBINANT HUMAN
; INTERFERON-BETA2
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/883,633

; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 208,925
; FILING DATE: 20-NOV-1980
; APPLICATION NUMBER: 449,447
; FILING DATE: 12-DEC-1989
; APPLICATION NUMBER: 860,883
; FILING DATE: 08-MAY-1986
; APPLICATION NUMBER: 208,925
; FILING DATE: 20-NOV-1980
; SEQ ID NO: 1:
; LENGTH: 1145
5510472-1

Query Match 35.0%; Score 563.6; DB:7; Length 1145;
Best Local Similarity 99.3%; Pred. No. 2.9e-136;
Matches 566; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1042 ccagttaccccgaggagagattccaaagatgtagcgcgccccacacagacagcactcacc 1101
DB 171 ccagttaccccgaggagagattccaaagatgtagcgcgccccacacagacagcactcacc 230
QY 1102 tcttcagaacgaattgacaaacaaattcgggtacatctctcgacgggcatctcagccctgaga 1161
DB 231 tcttcagaacgaattgacaaacaaattcgggtacatctctcgacgggcatctcagccctgaga 290
QY 1162 aaggagacatgtacaagagtaacatgtgtgaagcagcaagagagcactggcagaaaaac 1221
DB 291 aaggagacatgtacaagagtaacatgtgtgaagcagcaagagagcactggcagaaaaac 350
QY 1222 aacctgaacctccaaagatgctgaaagagtgatgcttccaatctcgtgattcaatgag 1281
DB 351 aacctgaacctccaaagatgctgaaagagtgatgcttccaatctcgtgattcaatgag 410
QY 1282 gagacttgctggtgaaatcatcactggtcttcttgagggttgagggtatcacctagagtac 1341
DB 411 gagacttgctggtgaaatcatcactggtcttcttgagggttgagggtatcacctagagtac 470
QY 1342 ctccagaacagattgagagtagtgaggaaacagcagagcagctgtgcagatgagtacaaa 1401
DB 471 ctccagaacagattgagagtagtgaggaaacagcagagcagctgtgcagatgagtacaaa 530
QY 1402 gtccgtgatccagtctcgcagaaaaggcaagaaatctagatgcaataaccacctgac 1461
DB 531 gtccgtgatccagtctcgcagaaaaggcaagaaatctagatgcaataaccacctgac 590
QY 1462 ccaaccacaaatgccagcctgctgcagagctgcagagctgcaggacagaaaccagtggtgcaggac 1521
DB 591 ccaaccacaaatgccagcctgctgcagagctgcagagctgcaggacagaaaccagtggtgcaggac 650
QY 1522 atgacaactcatctcattctgcagcgtttaaaggagttcctcagtcagcctgagggct 1581
DB 651 atgacaactcatctcattctgcagcgtttaaaggagttcctcagtcagcctgagggct 710
QY 1582 ctccgcaaatgacatgggcacccgtcga 1611
DB 711 ctccgcaaatgacatgggcacccctcaga 740

RESULT 7
US-08-437-680A-1
; Sequence 1, Application US/08437680A
; Patent No. 5681723
; GENERAL INFORMATION:
; APPLICANT: Ciliberto, Gennaro
; APPLICANT: Savino, Rocco
; TITLE OF INVENTION: Mutant Interleukin 6 with Improved
; TITLE OF INVENTION: Biological Activity Over Wild Interleukin 6
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch and Birch
; STREET: P.O. Box 747

; CITY: Falls Church
; STATE: VA
; COUNTRY: US
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,680A
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1264-133P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 555 base pair
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; DEVELOPMENTAL STAGE: Adult
; CELL TYPE: monocyte
; IMMEDIATE SOURCE:
; LIBRARY: CDNA
; CLONE: pB.B2.21
; US-08-437-680A-1

Query Match 34.2%; Score 551.8; DB 1; Length 555;
Best Local Similarity 99.6%; Pred. No. 2.5e-133;
Matches 553; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1042 ccagttaccccgaggagagattccaaagatgtagcgcgccccacacagacagcactcacc 1101
DB 1 CCAGTACCCCCAGGAGAGATTCCAAAAGATGTAGCGCCCCACACAGACAGCCACTCACC 60
QY 1102 tcttcagaacgaattgacaaacaaattcgggtacatctcgtcagcggcatctcagccctgaga 1161
DB 61 TCTTCAGAACGAATTGACAAACAATTCGGTACATCTCTCGACGGCATCTCAGCCCTGAGA 120
QY 1162 aaggagacatgtacaagagtagtaacatgtgtgaagcagcaagagagcactggcagaaaaac 1221
DB 121 AAGGAGACATGTAAACAAGAGTAACATGTGTGAAAGCAGCAAGAGAGGACTGGCAGAAAAAC 180
QY 1222 aacctgaacctccaaagatggtgaaagatggtgttccaatctcgtgattcaatgag 1281
DB 181 AACCTGAACCTTCCAAAAGATGGCTGAAAAGATGGTATCTCCAATCTCGATTCAATGAG 240
QY 1282 gagacttgctggtgaaatcatcactggtcttcttgagggttgagggtatcacctagagtac 1341
DB 241 GAGACTTGCTGTTGAAAATCATCTACTGTCTTTTGGAGTTTGAGGTATACCTTAGAGTAC 300
QY 1342 ctccagaacagattgagagtagtgaggaaacagcagagcagctgtgcagatgagtacaaaa 1401
DB 301 CTCACAGAACAGATTTGAGAGTAGTGAGGAAACAAGCCAGAGCTGTCCAGATGAGTACAAAA 360
QY 1402 gtccgtgatccagtctcgcagaaaaggcaagaaatctcagatgcaataaccacctgac 1461
DB 361 GTCCTGATCCAGTTCCTGCGAAAAAAGGGAATCTAGATGCAATAACACCCCTGAC 420
QY 1462 ccaaccacaaatgccagcctgctgcagagctgcagagcagcaagaaaccagtggtgcaggac 1521

Db 421 CCAACCAACAAATGCGAGCTGCTGACGAAGCTGCAGGCACAGAACCACTGGCTGCAGGAC 480
QY 1522 atgacaactcatctatctcgcagctttaaagaattccctcactccagctcagggct 1581
Db 481 ATGACAACACTCATCTCATCTCTCGGAGCTTTAAGGAGTTCTTGCAGCTCCAGGCTGAGGGCT 540
QY 1582 cttcgcaaatgtag 1596
Db 541 CTTGCGCAAAATGTAG 555
RESULT 8
US-07-745-382-19
; Sequence 19, Application US/07745382
; Patent No. 5270181
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: LaValle, Edward
; TITLE OF INVENTION: Peptide and Protein Fusions To
; TITLE OF INVENTION: Thioresoxin and Thioresoxin-Like Molecules
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/745,382
; FILING DATE: 19910814
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/652,531
; FILING DATE: 06-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseri, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: G15188A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..558
; US-07-745-382-19

Query Match 34.1%; Score 550.4; DB 1; Length 561;
Best Local Similarity 98.9%; Pred. No. 5.7e-133;
Matches 554; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1037 tcgagccagtcaccccgaggaagattccaaagatgacgcgccccacacagacagccac 1096
Db 2 TGGCTCAGTACCTCCAGGTGAAGATTCTAAAGATGTAGCGCGCCGCCACACAGAGCCAC 61
QY 1097 tcacctttcagaacgaattgacaacaaattcggtacatcctcgagcggtatctcagccc 1156
Db 62 TCACCTCTTCAGAACGAATTGACAAACAAATTCGGTACATCTCCTCGAGGGCATCTCAGCCC 121

QY 1157 tgaagaagagacatgtaacaagagtagtaactgtgtgaaagcagcaaaagagcactggcag 1216
Db 122 TGAGAAAGGAGACATGTAAACAGAGTAGTACATGTGTGAAAGCAGCAAGAGGCATGGCAG 181
QY 1217 aaaaacacctgaaaccttccaaagatggctgctgctgcttcccaatcttgattca 1276
Db 182 AAAACAACCTGAACCTTCCAAAGATGGCTGAAAAAAGATGGATGCTTCCAATCTGGATTCA 241
QY 1277 atgaggagactgctcgtgtaaaatcatcactgctgttttggagtttgaggtatcacctag 1336
Db 242 ATGAGGAGACTTGGCTGGTGAATAATCATCTGCTCTTTTGGAGTTTGGAGTATACCTAG 301
QY 1337 agtacctccagaacacagatttgagagtagtgaggaacagccagagctgtgcagatgagta 1396
Db 302 AGTACCTCCAGAACAGATTGAGAGTAGTAGGAGAACAGCCAGAGCTGTGCAGATGAGTA 361
QY 1397 caaagctctgctcagcttctcctgcagaaaaaggcaaaagaatctagatgcaataaccaccc 1456
Db 362 CAAAAGTCTGATCCAGTTCTTGCAGAAAAAGGCAAAAGATCTAGATGCAATAACCAACC 421
QY 1457 ctgacccaacacacaaatgccagcctgctgcagaaagctgcaggaacagacagacagtggtgc 1516
Db 422 CTGACCCCAACCAAAATGCCAGCCTGCTGACGAAGCTGCAGGAGCTGCAGAGCCAGTGGCTGC 481
QY 1517 aggacatgacaactcatctcattctgcagcctttaaaggagttcctcagtcagtcagcctga 1576
Db 482 AGGACATGACAACCTCATCTCATCTTGGCAGCTTTAAGGAGTTCTCGAGTCCAGCCTGA 541
QY 1577 gggctcttcggcaaatgtag 1596
Db 542 GGGCTCTTCGCAAAATGTAG 561
RESULT 9
US-07-921-848-19
; Sequence 19, Application US/07921848
; Patent No. 5292646
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: LaValle, Edward
; TITLE OF INVENTION: Peptide and Protein Fusions To
; TITLE OF INVENTION: Thioresoxin and Thioresoxin-Like Molecules
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/921,848
; FILING DATE: 19920728
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/652,531
; FILING DATE: 06-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,382
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseri, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: G15188A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..558
US-07-921-848-19

Query Match 34.1%; Score 550.4; DB 1; Length 561;
Best Local Similarity 98.9%; Pred. No. 5.7e-133;
Matches 554; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1037 tcagagcagttaccccccagagagattccaaagatgtagcgcgcacacagacagccac 1096
Db 2 TGGCTCCAGTACCTCCAGGTGAAGATTCTAAAGATGTAGCGCGCCACACAGACGCCAC 61
QY 1097 tcacctttcagacgaattgacaaacaaattcggtacatctctcgacgcatctcagccc 1156
Db 62 TCACCTCTTCAGAACGAATTGACAAACAATTCGGTACATCTCCGCGGCATCTCAGCCC 121
QY 1157 tgaaagaggagacatgtacaagtagtaacatgtgtgaaagcagcaaaagagcactggcag 1216
Db 122 TGAGAAAGGAGACATGTAAACAGAGTAACATGTGTGAAGCAGCAAAAGAGCGACTGGCAG 181
QY 1217 aaaaacacctgaaccttccaaagatggctgaaagagatggatcttccatctggattca 1276
Db 182 AAAACAACCTGAACCTTCCAAAGATGGCTGAAAAGATGGATGCTTCCAATCTGGATTCA 241
QY 1277 atgagagacttcctgggtgaaatacactcactgtcttttggagtttgaggtatacctag 1396
Db 242 ATGAGGAGACTTCGCTGGTGAATCATCTACTGCTCTTTGGAGTTTGAGGTATACCTAG 301
QY 1337 agtacctccagaaacagatttgagagtagtgaggaaacagcagagctgtgcagatgagta 1396
Db 302 AGTACCTCCAGAACAGATTTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTA 361
QY 1397 caaaagtcctgatcccttcctcagaaagagagagagagagagagagagagagagagagag 1456
Db 362 CAAAAGTCTTGATCCAGCTTCCAAAGATGGCTGAAAAGATGGATGCTTCCAATCTGGATTCA 241
QY 1457 aggacatgacaactcatctcattctgcgcagctttaaggagttcctgagtcagtcagcctga 1576
Db 482 AGGACATGACAACCTCATCTCATCTGCGCAGCTTTAAGGAGTTTCTGCAGTCCAGCCTGA 541
QY 1577 gggctcttcggcaaatgtag 1596
Db 542 GGGCTCTTCGGCAATGATAG 561

RESULT 10
US-08-165-301A-19
Sequence 19, Application US/08165301A
Patent No. 5646016
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: Dblasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: LaVallie, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
THIOREDOXIN-LIKE MOLECULES
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive

CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165.301A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meiner, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ. ID NO. 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..558
US-08-165-301A-19

Query Match 34.1%; Score 550.4; DB 1; Length 561;
Best Local Similarity 98.9%; Pred. No. 5.7e-133;
Matches 554; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1037 tcagagcagttaccccccagagagattccaaagatgtagcgcgcacacagacagccac 1096
Db 2 TGGCTCCAGTACCTCCAGGTGAAGATTCTAAAGATGTAGCGCGCCACACAGACGCCAC 61
QY 1097 tcacctttcagacgaattgacaaacaaattcggtacatctctcgacgcatctcagccc 1156
Db 62 TCACCTCTTCAGAACGAATTGACAAACAATTCGGTACATCTCTCGACGGCATCTCAGCCC 121
QY 1157 tgaaagaggagacatgtacaagtagtaacatgtgtgaaagcagcaaaagagcactggcag 1216
Db 122 TGAGAAAGGAGACATGTAAACAGAGTAACATGTGTGAAGCAGCAAAAGAGCGACTGGCAG 181
QY 1217 aaaaacacctgaaccttccaaagatggctgaaagagatggatcttccatctggattca 1276
Db 182 AAAACAACCTGAACCTTCCAAAGATGGCTGAAAAGATGGATGCTTCCAATCTGGATTCA 241
QY 1277 atgagagacttcctgggtgaaatacactcactgtcttttggagtttgaggtatacctag 1396
Db 242 ATGAGGAGACTTCGCTGGTGAATCATCTACTGCTCTTTGGAGTTTGAGGTATACCTAG 301
QY 1337 agtacctccagaaacagatttgagagtagtgaggaaacagcagagctgtgcagatgagta 1396
Db 302 AGTACCTCCAGAACAGATTTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTA 361
QY 1397 caaaagtcctgatcccttcctcagaaagagagagagagagagagagagagagagagagag 1456
Db 362 CAAAAGTCTTGATCCAGCTTCCAAAGATGGCTGAAAAGATGGATGCTTCCAATCTGGATTCA 241
QY 1457 aggacatgacaactcatctcattctgcgcagctttaaggagttcctgagtcagtcagcctga 1576
Db 482 AGGACATGACAACCTCATCTCATCTGCGCAGCTTTAAGGAGTTTCTGCAGTCCAGCCTGA 541

QY 1577 gggctcttcggcaaatgtag 1596
|||||
Db 542 GGGCTCTTCGGCAAAATGTAG 561

RESULT 11

PCT-US94-14179-19
; Sequence 19, Application PC/TUS9414179
; GENERAL INFORMATION:
; APPLICANT: McCov, John
; APPLICANT: DiBlasio-Smith, Elizabeth
; APPLICANT: Grant, Kathleen
; APPLICANT: LaVallie, Edward R.
; TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
; THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
; THIOREDOXIN-LIKE MOLECULES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14179
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weinert, M. C. 33,544
; REGISTRATION NUMBER: GI 5188D
; REFERENCE/DOCKET NUMBER: GI 5188D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..558

PCT-US94-14179-19

Query Match 34.1%; Score 550.4; DB 6; Length 561;
Best Local Similarity 98.9%; Pred. No. 5.7e-133;
Matches 554; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1037 tcgagccgtaccgccaggaagattccaaagatgtagccgccccacacagacagccac 1096
|||||
Db 2 TGGCTCCAGTACTCCAGTGAAGATTCTAAGATGTAGCCGCCCCACACAGACAGCCAC 61
QY 1097 teacctcttcagaacgaattgacaacaaattcgtatcatctcgcagcgcatctcagccc 1156
|||||
Db 62 TCACCTCTTCAGAACGAATTGACAAACAAATTCGTATCATCTCGACGGCATCTCAGCCC 121
QY 1157 tgagaaaggagacatgtacaagagtaacatgtgtgaaagcagcaaaaggagcactggcag 1216
|||||
Db 122 TGAGAAAGGAGACATGTAAACAGAGTAACATGTGTGAAAGCAGCAAAAGAGGCACTGGCAG 181
QY 1217 aaaaacacctgaacctccaaagatggctgaaaagatggatgtccaatcttgattca 1276
|||||
Db 182 AAACAACCTGAACCTTCCAAAGATGGCTGAAAGAAGATGGATGCTTCCAAATCTGGATTCA 241

QY 1277 atgaggagacttcctgggtgaaaaatcatcactcgtctcttttgagtttgaggtatacctag 1336
|||||
Db 242 ATGAGGAGACTTGCCTGGTGAAAATCATCATCTGGTCTTTTGGAGTTTGGAGTTACCTAG 301
QY 1337 agtacctccagaacagatttgagagtagtgaggaacaaagccagagctgtgcagatgagta 1396
|||||
Db 302 AGTACTCCAGAACAGATTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTA 361
QY 1397 caaaagtctgatccagttccttcgagaaaaagcaaaagaaatctagatgcaataaacaccc 1456
|||||
Db 362 CAAAAGTCTGTATCCAGTTCCTTCGAGAAAAGGCAAAAGAAATCTAGATGCAATTAACACCC 421
QY 1457 ctgaccccaaccacaatgccagctgcctgcagaaagctgcagacacagacagactgagctgc 1516
|||||
Db 422 CTGACCCCAACCAAAATGCCAGCCCTGCTGACGAAGCTGCAGGCACAGAACCACTAGTGGCTGC 481
QY 1517 aggcacatgacaaactcatctcctgcgcagctttaaagagttcctgcagtcacagccctga 1576
|||||
Db 482 AGGACATGACAACTCATCTCATCTTCGCGCAGCTTTAAGGAGTTCCTGCAGTCCAGCCTGA 541
QY 1577 gggctcttcggcaaatgtag 1596
|||||
Db 542 GGGCTCTTCGGCAAAATGTAG 561

RESULT 12

US-08-469-318-57
; Sequence 57, Application US/08469318
; Patent No. 6022535
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 196
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,318
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,872
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 951 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-469-318-57

Query Match 33.4%; Score 538.6; DB 5; Length 951;
Best Local Similarity 95.0%; Pred. No. 7.6e-130;
Matches 556; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1009 ggtggaggttcttgaggtggaggttctgtcgagccagttaccgccagagagattccaaa 1068
|||||
Db 367 GGTGGTGTCTCTGGGGGGCTCCACATGGCTCCAGTACCACAGGTGAGATTCCAAA 426
QY 1069 gatgtagccgccccacacagacagaccactcctcttcagaaacgaattgacaaacaaatt 1128
|||||
Db 427 GATGTGGCGGCCCCACACAGACAGCCACTCCTCTTCAGAACGAATTCAGAACAAAT 486
QY 1129 cgtgtacatcttcgagcgcattctcagcctgagaagagacatatcaacagagtaacatg 1188
|||||
Db 487 CGGTACATCTTCGACGGGATATACGCTTGAAGAGGAGACATGTAAACAGAGTAACATG 546
QY 1189 tgtgaaagcagcaaaaggaggtgaggtgagcaaaacacctgaaccttccaaagatggctgaa 1248

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Db 547 TGTGAAGCAGCAAGAGGCGCTAGCAGAAAAACAACCTGAACCTTCCAAAGATGGCTGAA 606
QY 1249 aaagatgagatcttcaaatctgattcaatgagagagacttgcctggtgaaatcatcaact 1308
Db 607 AAGATGGATGCTTCCAAATCCGATTCATGAGGAGACTTGCCTGTGTGAAATTCATCACT 666
QY 1309 ggtctttgagttgaggtatatactagatgactccagaaacagatttggagagtagtgag 1368
Db 667 GGTCTTTTGGAGTTTGGAGTTATACCTCGAGTACTCCAGAACAGATTGAGAGTAGTGAG 726
QY 1369 gaacaagccagagctgtgcagatgagtagacaaagtctcctgagtagtccctgcagaaaaag 1428
Db 727 GAACAAGCCAGAGCTGTGCAGATGTGCACAAAAGTCTGTATCCAGTTCCTGTCAGAAAAAG 786
QY 1429 gcaagaatactagatgaataaaccaccctgaccacaacacaaatgccagcctgctgagc 1488
Db 787 GCAAGAATCTAGATGCAATTAACACCCCTGACCCCAACCAATGCATCCCTGCTGAGC 846
QY 1489 aagctgcagcagacagaccagtgctgcagagacatgacaaactcatctcattctgcgcagc 1548
Db 847 AAGCTGCAGCAGACAGACAGTGGCTGCAGGACATGACAACTCATCTCATCTTCTGCGCAGC 906
QY 1549 tttaaggagttcctgcagtcagcctgagggctctcttgcggcaaatg 1593
Db 907 TTTAAGGAGTCTCGAGTCCAGCTGAGGGCTCTTCGGCAAAATG 951

RESULT 13
PCT-US95-01185-57
; Sequence 57, Application PC/TUS9501185
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
; NUMBER OF SEQUENCES: 196
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01185
; FILING DATE: 02-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192325
; FILING DATE: 14-FEB-1994
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 951 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-01185-57

Query Match 33.4%; Score 538.6; DB 6; Length 951;
Best Local Similarity 95.0%; Pred. No. 7.6e-130;
Matches 556; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1009 ggtggaggttctggaggtgaggttctgtcgagccagtagccccccagagagattccaaa 1068
Db 367 GGTGGTGGTGTCTGGCGCGCTCCAAATGGCTCCAGTACCAACAGAGGTGAAGATTCCAAA 426
QY 1069 gatgagccgccccacacagacgactcacctcttcagaaagattgacaacaaatt 1128
Db 427 GATGTGGCGCGCCCCACACAGACAGCCACTCACCTCTTCAGAACGAATTGACAAACAATT 486
QY 1129 cggtagatcctcgacggcatctcagcctcgagaaagagagcatgtaacaagagtaaatg 1188
Db 487 CGGTACATCTCGACGGGATATCAGCCCTCAGAAAGGAGACATGTAAACAGAGTAAATG 546
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QY 1189 tgtgaagcagcaagagggcactggcagaaaaaacctgaaccttccaaagatggctgaa 1248
Db 547 TGTGAAGCAGCAAGAGGCGCTAGCAGAAAAACAACCTGAACCTTCCAAAGATGGCTGAA 606
QY 1249 aaagatgagatcttcaaatctgattcaatgagagagacttgcctggtgaaatcatcaact 1308
Db 607 AAGATGGATGCTTCCAAATCCGATTCATGAGGAGACTTGCCTGTGTGAAATTCATCACT 666
QY 1309 ggtctttgagttgaggtatatactagatgactccagaaacagatttggagagtagtgag 1368
Db 667 GGTCTTTTGGAGTTTGGAGTTATACCTCGAGTACTCCAGAACAGATTGAGAGTAGTGAG 726
QY 1369 gaacaagccagagctgtgcagatgagtagacaaagtctcctgagtagtccctgcagaaaaag 1428
Db 727 GAACAAGCCAGAGCTGTGCAGATGTGCACAAAAGTCTGTATCCAGTTCCTGTCAGAAAAAG 786
QY 1429 gcaagaatactagatgaataaaccaccctgaccacaacacaaatgccagcctgctgagc 1488
Db 787 GCAAGAATCTAGATGCAATTAACACCCCTGACCCCAACCAATGCATCCCTGCTGAGC 846
QY 1489 aagctgcagcagacagaccagtgctgcagagacatgacaaactcatctcattctgcgcagc 1548
Db 847 AAGCTGCAGCAGACAGACAGTGGCTGCAGGACATGACAACTCATCTCATCTTCTGCGCAGC 906
QY 1549 tttaaggagttcctgcagtcagcctgagggctctcttgcggcaaatg 1593
Db 907 TTTAAGGAGTCTCGAGTCCAGCTGAGGGCTCTTCGGCAAAATG 951

RESULT 14
PCT-US94-12873-3
; Sequence 3, Application PC/TUS9412873
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HYBRID CYTOKINES
; NUMBER OF SEQUENCES: 26
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44Mb, double side, high density
; OPERATING SYSTEM: MS-DOS Version 6
; SOFTWARE: WORD for WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12873
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
PCT-US94-12873-3

Query Match 33.4%; Score 538.4; DB 6; Length 540;
Best Local Similarity 99.8%; Pred. No. 6.9e-130;
Matches 539; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1057 gaagatcccaagatgtagcgccccacagacagcactcacctcttcagaaacgaatt 1116
Db 1 GAAGATTCCAAAGATGTAGCGCGCCCCACACAGACAGAGCCACTCACCTTTCAGAACGAATT 60
QY 1117 gacaaacaaatcggtatcctctgcagcgcatctcagccctgagaaaggagacatgtaac 1176
Db 61 GACAAACAAATTCGGTACATCTCTCGCGGCATCTCAGCCCTGAGAAAGGAGACATGTAAC 120
QY 1177 aagatgaatgtagtgaagcagcaagagagcactggcagaaaaaacacctgaacctcca 1236
Db 121 AAGAGTAAATGTGTGAAGCAGCAAAAGAGGCACTGGCAGAAAAACAACCTGAACCTTCCA 180
QY 1237 aagatgctgaaaaagatgagtgcttccaatctgattcaatgagagacttgcctggtg 1296
```


Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	1587	98.4	1627	1	T97848	Human fusion polyp	
2	1482	91.9	1552	1	T97849	Human fusion polyp	
3	995	61.7	2061	1	N90340	Sequence encoding	
4	995	61.7	2066	1	Q41746	IL-6 receptor codi	
5	995	61.7	2087	1	N90847	DNA contg. region	
6	995	61.7	3319	1	V60296	Human interleukin-	
7	993.4	61.6	1486	1	V60296	Human interleukin-	
8	993.4	61.6	3319	1	T31441	Interleukin-6 rece	
9	969	60.1	1074	1	V04440	Interleukin 6 rece	
10	565.2	35.1	1139	1	N90255	Interleukin-6. New	
11	565.2	35.1	1139	1	N80299	Interleukin 6. Pro	
12	565.2	35.1	1162	1	Q01763	BSF-2 gene for hum	
13	563.6	35.0	1101	1	N90131	DNA sequence of pB	
14	563.6	35.0	1101	1	N90135	DNA sequence of pB	
15	563.6	35.0	1101	1	N90345	Plasmid pBSF2-L8.	
16	563.6	35.0	1128	1	Q74057	Human interleukin	
17	563.6	35.0	1128	1	V60294	Human interleukin-	
18	563.6	35.0	1145	1	N90377	Interferon-beta-2	
19	563.6	35.0	1145	1	N70348	Sequence of human	
20	563.6	35.0	1145	1	Q39582	IFN-beta-2a coding	
21	563.6	35.0	1145	1	Q86523	cdNA encoding inte	
22	563.6	35.0	1161	1	N81460	Sequence encoding	
23	562	34.9	1101	1	N80966	Plasmid pBSF2-L8.	
24	562	34.9	1101	1	N81517	Sequence encoding	
25	558.8	34.7	1099	1	Q25831	Mutant human BCDF.	
26	558	34.6	1165	1	Q56265	Sequence of human	
27	555	34.4	639	1	N91706	Human interleukin-	
28	554	34.4	1162	1	Q11824	B cell differentia	
29	552.2	34.3	566	1	N80300	Interleukin 6. Pro	
30	551.8	34.2	555	1	Q65465	Mutant Interleukin	
31	550.4	34.1	561	1	Q56903	Human Interleukin	
32	550.4	34.1	561	1	Q09773	Human interleukin-	
33	549	34.1	560	1	Q03365	Segment of human B	

Qy	1021	ggagtgtaggtttctgtcgagccagtcacccccaggaggaagtatccaaagatgtagccgcc	1080
Db	961	GGAGGTGGAGGTTCTGTCTCGAGCCAGTACCCCCAGGAGAAGATTCCAAGATGTAGCCGCC	1020
Qy	1081	ccacagacagccactcaactcttcagaaacaaattgacaaacaattcggtacatcttc	1140
Db	1021	CCACACAGACAGCCACTCACTCTTCAGAACGAAATGTGACAAACAATTCGGTACATCCTC	1080
Qy	1141	gacggcatctcagccctcgagaagaagagacatgtaaacaagtgtaacatgtgtgaaagcagc	1200
Db	1081	GACGGCATCTCAGCCCTCGAGAAAGGAGACATGTAAACAAGTAGTGTGTGAAAGCAGC	1140
Qy	1201	aaagagcactgcagcaaaaaaaccttgaaccttccaaagatggctgaaaaagatggtatgc	1260
Db	1141	AAAGAGCCTTGGCAGAAAAAACCTTGAACCTTCCAAAGATGGCTGAAAAAGATGGATGC	1200
Qy	1261	ttcaactctgattcaatagagagacttgcctgggtgaaaatacatcactggtcttttgag	1320
Db	1201	TTCCAAATCTGGATTCAATGAGGAGACTTGCCTGGTGAAATCATCACCTGGTCTTTTGGAG	1260
Qy	1321	tttgaggtatacttagtactctccagaaacagatttgagagtagtgagagaaacaagccaga	1380
Db	1261	TTTGAGGTATACCTAGAGTACCTCCAGAACAGATTGAGAGTAGTGAGSACAAGCCAGA	1320
Qy	1381	gctgtcagatgtagtcaaaagtctctgtatccagtttcttcagaaaaagcgaagaatcta	1440
Db	1321	GCTGTGCAGATGAGTACAAAAGTCTGTGATCCAGTTCCTCTCAGAAAAAGCAAGAATCTA	1380
Qy	1441	gatcgaataaccacccctgacccaacacacaaatgccagctctgcacgaagctgcaggca	1500
Db	1381	GATGCAATATACCACCCCTGACCCAAACCAAAATGCCAGCTCTCAGCAAGCTGCAGGCA	1440
Qy	1501	cagaaaccagtggctgcaggacatgacaactcatcttctcgcagcttttaaggagttc	1560
Db	1441	CAGAACCAAGTGGCTGCAGGACATGACAACTCATCTTCCTCGGAGCTTTAAGAGTTC	1500
Qy	1561	ctgcagtcagctgaggggctcttcggcaaatgtagcatggcgaccctcgac 1612	
Db	1501	CTGCAGTCCAGCCTGAGGGGCTCTTCGGCAAAATGTAGCATGGGACCGTCGAC 1552	
RESULT 3			
FN	N90340		
ID	N90340 standard; cDNA; 2061 BP.		
AC	N90340;		
DT	31-MAR-1992 (first entry)		
DE	Sequence encoding a receptor protein for human B cell stimulating		
DE	factor-2 (BSF2 receptor).		
KW	B cell; immune disorder; therapy; diagnosis; prophylaxis; ss.		
OS	Homo sapiens.		
FX	Key	Location/Qualifiers	
FT	cds	247..1153	
FT		/tag= a	
FT		/note= "SQ claimed"	
FN	EP-325474-A.		
PD	26-JUL-1989.		
PF	20-JAN-1989; 300536.		
PR	22-JAN-1988; JP-012387.		
PR	25-JAN-1988; JP-012599.		
PR	04-AUG-1988; JP-194885.		
PR	14-JAN-1989; JP-017461.		
PR	20-JAN-1989; JP-009774.		
PA	(KISH/) KISHIMOTO T.		
PI	Kishimoto T.		
DR	WPI; 89-214667/30.		
DR	P-PSDB; P90284.		
PT	Receptor protein for human B cell stimulating factor-2 - obt'd. by		
PT	recombinant DNA techniques and used as diagnostic, prophylactic or		
PT	therapeutic agent		
FS	Disclosure; Fig 3; 63pp; English.		
CC	The cDNA in N90340 was derived from monocyte cell line U937.		
CC	Isolated BSF2 receptor and DNA encoding it are claimed, as are		
CC	(b) expression vectors; (c) host organisms; (d) antibodies; and		

QY 488 agtttcagaaacagtcgcccgaagacttccagagccgtgcccagtgatcccccagtgccc 547
DB 680 AGTTTCAGAAACAGTCGCGCGGAAGACTTCCAGGAGCGGTGCCAGTATTCACAGAGTCCC 739
QY 548 aqaagtctcctgcacagttagcagtcctcccgaggagacagctcttctacatagtgcca 607
DB 740 AGAAGTTCCTCCTGCCAGTTAGCAGTCCCGAGGAGACAGCTCTTTCTACATAGTCCCA 799
QY 608 tctggtcccgagtcagtgctcggagcaagttcagcaaaaactcaaacctttcaggggttg 667
DB 800 TGTGCGTCCCGAGTAGTGTGCGGAGCAAGTTACAGAAAACCTCAAACTTTACAGGTTGTG 859
QY 668 gaactctgcagctgatccgcctgccaaacatcacagtcactgcgctggtggccagaaaccccc 727
DB 860 GAATCTTGACGCTGATCCGCTGCCAACATCACAGTCACTGCCGTGGCCAGAAACCCCC 919
QY 728 gctggtcagtgctcactggtcagagccccccactcctcgtggaactcacttctacagactac 787
DB 920 GCTGGCTCAGTGTCACTGGCAAGAGCCCCACTCTCTGGAACATCATCTTTCTACAGACTAC 979
QY 788 gtttgagctcagatcggcgtgaacgtcaagcgtcaagacattcacacatggtgtcaagg 847
DB 980 GGTTTGAGCTCAGATATCGGGCTGAACGGTCAAGACATTCACAACTGGATGGTCAAGG 1039
QY 848 acctccagatcactgtgtcattccacgacgctggtgagcgcctgagggcagctggtgcagc 907
DB 1040 ACCTCCAGCATCACGTGTTCATCCAGACGCGCTGGAGCGGCTGAGCGACGTGGTGCAGC 1099
QY 908 ttcgtgccagagaggttcgggcaaggcgagtggtgagcagtggtgagccggagggccatgg 967
DB 1100 TTCGTGCCAGGAGGAGTTCGGGCAAGGCGAGTGGAGCGAGTGGAGCCGGAGGCCATGG 1159
QY 968 gcacgcttgacagaatccagagtcctccagct 1002
DB 1160 GCACGCTTGGACAGAATCCAGAGTCTCTCCAGCT 1194

RESULT 5
ID N90847
AC N90847 standard; DNA; 2087 BP.
DT 23-JAN-1990 (first entry)
DE DNA contg. region encoding BSF2 receptor.
KW B cell stimulating factor-2 receptor; monocyte U937 cell line.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 247..1650
FT misc_feature /*tag= a
FT FT 250..312
FT FT /*tag= b
FT FT 1330..1404
FT FT /*tag= c
PN AU8928720-A.
PD 27-JUL-1989.
PF 23-JAN-1989; 28720.
PR 22-JAN-1988; JP-012387.
PR 25-JAN-1988; JP-012599.
PR 04-AUG-1988; JP-194885.
PR 14-JAN-1989; JP-007461.
PA (KISH) Tadamoto Kishimoto.
PI Kishimoto T;
DR WPI; 89-264012/37, P-PSDB; P90525.
PT Receptor protein for human B cell stimulating factor-2 - used for
PT developing prophylactic, therapeutic and diagnostic agents for
PT associated disorders.
PS Disclosure; fig 3.1-3.5; 76pp; English.
CC The DNA contains a region encoding the BSF2 receptor derived from a
CC monocyte U937 cell line. It is used to produce large amts. of receptor,
CC and may also be used as a probe for screening related genes.
CC Regions b and c represent N- and C-terminal hydrophobic regions resp.
SQ Sequence 2087 BP; 426 A; 646 C; 621 G; 394 T;

Query Match 61.7%; Score 995; DB 1; Length 2087;
Best Local Similarity 100.0%; Pred. No. 5e-246;
Matches 995; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 catgagtgtagccagaggaggaagcatgctggcgtcgcgctgcgctgctgctgctgccc 67
DB 221 CATGGAGTGTAGCCGAGAGGAAGCATGCTGGCCGTGGCGTGGCGCTGCTGGCTGCC 280
QY 68 tgtgtgcccgcgcgggagcgcgctggcccccagggcgctccctgcgcagagagtgcaaa 127
DB 281 TGTGTGCCGCGCGGGAGCGCGCTGGCCCAAGCGCTGCCCTGCGCAGAGAGTGGCAA 340
QY 128 gagcgctgctgaccagctctccagggagacagctgactctgacctgcccgggggtagagc 187
DB 341 GAGCGGTGCTGACCACTCTGCCAGGAGACAGCTGACTCTGACTGCCCCGGGGTAGAGC 400
QY 188 cggaaacaaatgccactgttctactgggtgctcaggaagcggtgcagggtccccaccccc 247
DB 401 CGGAAGACAAATGCCACTGTTCACCTGGGTGCTCAGGAAGCGCGCTGCCAGGCTCCCACCCCCA 460
QY 248 gcagatgggtgcatgggaaggaggtgctgctgaggtcggtgcagctccacagactctg 307
DB 461 GCAGATGGGTGTCATGGGAAGGAGGCTGCTGTGAGGTGCGTSCAGCTCCACGACTCTG 520
QY 308 gaaactattcatctacccggcgccgcccagctgggactgtgaccttgccttgcgtggtgatg 367
DB 521 GAAACTATTTCATGCTACCGGGCGCGGCCGCCAGCTGGGACTGTGCATTTGCTGTGGATG 580
QY 368 tccccccaggagccccagctctctctcgttccgggaagagccccctcagcaatgttttt 427
DB 581 TTCCCCCGAGGAGCCCCAGCTCTCTCTGCTTCCGGAAGAGCCCCCTCAGCAATTTGTTT 640
QY 428 gtgagtggtgctcctggagcacccccatccctgacgacaaaggctgtccttctggtgagga 487
DB 641 GTGAGTGGGTCTCTCGAGACACCCCCATCCCTGAGACAAAAGGCTGTCTTGTGTGAGGA 700
QY 488 agtttcagaaacagtcgcccgaagacttccagagccgtgccagtatccccagagtgccc 547
DB 701 AGTTTCAGAAACAGTCGCGCGGAAGACTTCCAGGAGCGGTGCCAGTATTCACAGAGTCCC 760
QY 548 agaagttctcctgccagttagcagtcgcccggagggagagcagctcttctacatagtgcca 607
DB 761 AGAAGTTCCTCCTGCCAGTTAGCAGTCCCGAGGAGAGACAGCTCTTTCTACATAGTGTCCA 820
QY 608 tgtgctgcgcagtagtgctgggagcaagttcagcaaaactcaaacctttcaggggttggt 667
DB 821 TGTGCGTCCGCCAGTAGTGTCTGGGAGCAAGTTCAGCAAAACTCAAACTTTTCAGGGTTGTG 880
QY 668 gaatcttgacgctgatccgcctgccaaacatcacagtcactgcccgtgcccagaaaccccc 727
DB 881 GAATCTTGACGCTGATCCGCTGCCAACATCACAGTCACTGCGCTGGCCAGAAACCCCC 940
QY 728 gctggctcagtgctcactggtggaagacccccactcctcctggaactcatcttctacagactac 787
DB 941 GCTGGCTCAGTGTCACTGGCAAGACCCCCACTCTCTGGAACCTCATCTTTCTACAGACTAC 1000
QY 788 ggttgagctcagatcctggggtgaaacgtgcaagacattcaaacatgagtggtcaagg 847
DB 1001 GGTTTGAGCTCAGATATCGGGCTGAACGGTCAAGAGACATTCACAACTGGATGGTCAAGG 1060
QY 848 acctccagatcactgtgtcatccagacgctggagcgctcctgagcgactggtgctgagc 907
DB 1061 ACCTCCAGCATCACTGTGTCTATCCAGACGCTGGAGCGGCTGAGGACAGTGTGTGAGC 1120
QY 908 ttcgtgccagagaggttcgggcaaggcgagtggtgagcgagtcggagccccggagggccatgg 967
DB 1121 TTCGTGCCAGGAGAGTTCGGGCAAGGCCAGTGGAGCGAGTGGAGCCCGGAGGCCCATGG 1180
QY 968 gcacgcttgacagaatccagagtgctcctcagct 1002
DB 1181 GCACGCTTGGACAGAATCCAGGAGTCTCTCCAGCT 1215

Db	926	TTCTGTGCCAGGAGGAGTTCCGGCAGGCGAGTGGACCGAGGAGCCATGG	985
Qy	968	gcacgccttgacagaatccaggagtgctcctaagct	1002
Db	986	GCAGCGCTTGACAGAGATCCAGGAGTCTCCAGCT	1020
RESULT	8		
T31441			
ID	T31441	standard; cDNA; 3319 BP.	
AC	T31441		
DT	28-NOV-1996	(first entry)	
DE	Interleukin-6 receptor coding sequence.		
KW	Interleukin-6; IL; receptor; antisense oligonucleotide; inhibition;		
KW	gene expression; kidney tumour; myeloma; Kaposi's sarcoma; psoriasis;		
KW	rheumatoid arthritis; endotoxic shock; ss.		
OS	Homo sapiens.		
PH	Key	Location/Qualifiers	
FT	cds	438..1844	
FT	FT	/*tag= a	
FT	FT	/product= Interleukin-6 receptor.	
PN	W09618416-A1.		
PD	20-JUN-1996.		
PF	15-DEC-1995; J02587.		
PR	16-DEC-1994; JP-213167.		
PR	18-AUG-1995; JP-210739.		
PA	(CHUS) CHUGAI SEIYAKU KK.		
PI	Koishibara Y, Kuromaru K;		
DR	WPI; 96-300392/30.		
DR	P-PSDB; R98364.		
PT	Anti-sense oligo:nucleotide inhibitor against human IL-6R expression		
PT	- for treatment of e.g. tumours, cancers, rheumatoid arthritis,		
PT	psoriasis, endo:toxic shock, etc.		
PS	Claim 2; Page 17-21; 32pp; Japanese.		
CC	Antisense oligonucleotides may be used to inhibit the expression of		
CC	the interleukin-6 receptor. Inhibition of expression of the		
CC	IL-6 receptor is useful in the treatment of kidney tumours, myeloma,		
CC	Kaposi's sarcoma, rheumatoid arthritis, psoriasis and endotoxic		
CC	shock. The antisense oligonucleotides are administered at a dosage		
CC	of 0.1-100mg/kg, pref. 0.1-50 mg/kg,		
SC	Sequence 3319 BP; 735 A; 937 C; 960 G; 687 T;		
Query Match	61.6%;	Score 993.4;	DB 1; Length 3319;
Best Local Similarity	99.9%;	Pred. No. 1.6e-245;	
Matches	994;	Conservative 0;	Mismatches 1; Indels 0; Gaps
Qy	8	catgagtggtagccgaggaggaagcatgtgcccgtgcgctgcgctgcgctgcgctgcgc	67
Db	412	CATGAGTGTGTAGCCGAGGAGAAAGCATGCTGGCGCTCGGCTGCGCGCTGCTGCTGCC	471
Qy	68	tgtctgcccgcgggagcggcgtgccccaaaggcactccctgcagagagtgcaa	127
Db	472	TGCTGGCGCGCCGGGAGCGCGCTGGCCCCAAGGCGCTGCCCCGCGAGAGTGCCAA	531
Qy	128	gagcgctgtgaccagttctgcaggagacacgctgactctgacctgcccggggtagagc	181
Db	532	GAGCGTGCTGACCAGCTGTGCGAGGACACACGCTGACTCTGACCTGCCCGGGGTAGAGC	591
Qy	188	cgaagacaatgccactgttcactgggttgctcaggaagcggctgcaggtccaccacca	247
Db	592	CGGAAGACAATGCCACTGTTCACTGGTGTCTCAGGAAGCGGCTGCAGGCTCCACCCCA	651
Qy	248	gcagatgggtcgcatgggaagaggtgctgctgtagggtcggtgcagctccagactctg	307
Db	652	GCAGATGGGCTGGCATGGGAAGAGAGGCTGCTGTGTAGGTGGGTGCAGCTCCACACTGT	711
Qy	308	gaactattcatgctacccggcggccgccagctggagactgtgacctgtgctgtggtgatg	367
Db	712	GAACATAATCAATGCTACCGGGCCGGCCGCCAGCTGGGACTGTGCTGCTGGTGATG	771
Qy	368	tccccccgagagaccgccagctctctctgcttcccgggaagagccccctcagaaattgttt	427

Db	841	GAGCCCTGGAGCGCGCTGAGGCACGTGTGTGCAGCTTCTGTGCCAGGAGGAGCTTCGGCGAA	900
Qy	934	ggcgagtgagcgagtgagcgagcccgaggccatgggcacgccttggacagaatccagaggt	993
Db	901	GGCGAGTGGAGCGAGTGGAGCCCGGAGGCCATGGGCACGCCTTGGACAGAAATCCAGGAGT	960
Qy	994	ctctcagct 1002	
Db	961	CCTCCAGCT 969	
RESULT 10			
N90255			
ID	N90255 standard; DNA; 1139 BP.		
AC	N90255;		
DT	1-NOV-1989 (first entry)		
DE	Interleukin-6.		
KW	Interleukin-6; lysine-depleted variant; site-directed		
OS	mutagenesis; human.		
KW	Homo sapiens		
Key	Location/Qualifiers		
FT	51..686		
FT	cds		
FT	/*tag= a		
PN	W08905824-A.		
PD	29-JUN-1989.		
PF	22-DEC-1988; U04633.		
PR	23-DEC-1987; US-137043.		
PA	(GENE) Genetics Inst Inc.		
PI	Shaw G.		
DR	WPI; 89-206594/28.		
DR	P-PSDB; P90469.		
PT	New lysine depleted variants of polypeptide		
PT	- opt. modified with hydrophilic residues,		
PT	biologically active but with altered solubility, stability etc.		
PS	Disclosure, fig 3; 35pp; English.		
CC	DNA of interleukin-6 (see corresp. P90469). Used in the patent		
CC	to create lysine depleted variants by site-directed mutagenesis, or		
CC	synthesis.		
SQ	Sequence. 1139 BP; 361 A; 240 C; 231 G; 307 T;		

Query Match 35.1%; Score 565.2; DB 1; Length 1139;
Best Local Similarity 99.5%; Pred. No. 7.6e-136;
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1042	ccagttacccccaggagaaattccaagaatgtagccgcccacacacagacagccaactcacc	1101
Db	135	CCAGTACCCCCAGGAGAAGATTCCAAGATGTAGCGCGCCACACAGACAGCAGCAGCTCACC	194
Qy	1102	tcttcagaacgaattgacaaaacaaattcggttacattctctgcagcgcatctcagccctgaga	1161
Db	195	TCTTCAGAACGAATTGACAAACAAATTCGGTACATCTCTCGACGGCATCTCAGCCCTGAGA	254
Qy	1162	aaggagacatgtatacaagagtagtaactgtgtgaagcagcaagaaggcgacgtgacgaaaaac	1221
Db	255	AAGGAGACATGTAAACAAGAGTAACATGTGTGAAGCAGCAAGAGGACATGGCAGAAAAC	314
Qy	1222	aaactgaaccttccaaagatggctgaaaagaatgagatgcttccaaatctggattcaatgag	1281
Db	315	AACCTGAACCTTCCAAGATGGCTGAAAAAGATGGATGCTTCCAATCTGGATTCAATGAG	374
Qy	1282	gagacttgctggtgaaaaatactaactgctcttttggaggttggagggtatacactagaagtac	1341
Db	375	GAGACTTGCTGGTGAAAAATCATCATCTGCTCTTTTGGAGTTTGAGGTATACCTAGAGTAC	434
Qy	1342	ctccagaacagatttgagagtagtgaggaaacaagccagagctgtgcagatgagtacaaaaa	1401
Db	435	CTCCAGAACAGATTTCAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAAA	494
Qy	1402	gtcctgatccagtttctctgcagaaaaaaggcaaaagaatctagatgaaataaccacccctgac	1461
Db	495	GTCTGATCCAGTTCCTGCAGAAAAAGCCAAAGAACTCFAGATGCAATTAACCAACCCCTGAC	554

Query Match 35.1%; Score 565.2; DB 1; Length 1139;
Best Local Similarity 99.5%; Pred. No. 7.6e-136;
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1042	ccgataccccagagagaagattccaaagatgtagccgccccacacagacagcactcaacc	1101
Db	135	CCAGTAGCCCCAGAGAGAAGATTCCAAAGATTAGCGGCCCCACACAGACGCCACTCACC	194
Qy	1102	tcttcagaagaattgacaaacaaattcgttacatctcgacgcacatctcagccctgaga	1161
Db	195	TCCTTCAGAACGAATTGACAAACAATTTCGGTACATCTCTGACGGCGATCTCAGCCCTGAGA	254
Qy	1162	aaggagacatgtaacaagagtagtaacatggtgaaagcagcaaaagcagcactggcgagaaaaac	1221
Db	255	AAGGAGACATGTAACAAGAGTAACATGTGTGAAAGCAGCAAAAGAGGCACCTGGCAGAAAAAC	314
Qy	1222	aacctgaaccttcaagatggtctgaaaagatggatgtcttccaatctggtattcaatgag	1281
Db	315	AACCTGAACCTTCCTCAAGATGGCTTGAAAAGATGGATGCTTCTCCAATCTGGATTCAATGAG	374
Qy	1282	gagactgcctgggtgaaaaatcatcactcgtgtcttttgaggtttgaggtatacctagatgac	1341
Db	375	GAGACTTGCCCTGGTGGAAAATCATCACCTGGTCTTTTGGAGTTTGAGGTATACCTAGAGTAC	434

[illegible]

RESULT 11

8N0299	ID	N80299 standard; cDNA; 1139 BP.
AC	N80299;	
AC	08-OCT-1990 (first entry)	
DT	Interleukin 6.	
KW	IL-6; interleukin; cancer; ss.	
FW	Key	Location/Qualifiers
FT	cds	51..689
FT		/*tag= a
FT	signal_peptide	51..133
FT		/product=IL-6
FT		/*tag= b
FT	mat_peptide	132..686
FT		/*tag= c
PN	W08800206-A.	
PD	14-JAN-1988.	
PD	07-JUL-1987; U01611.	
PF	08-JUL-1986; US183207.	
PR	(GENE-) Genetics Inst Inc.	
PA	Clark SC Wong GG, Schendel P, McCoy J;	
PI	WPI; 88-021566/03.	
DR	P-PSDB; F80269.	
DR	Prodn. of non-glycosylated IL-6 - for use	
PT	disorders in haematopoietic cells and in	
PS	Disclosure; p; English.	
PT	The sequence is carried by pCSF309 in E.	
CC	ExoRI insert. It can be excised and used	
CC	plasmid for prodn. of IL-6. Bacterially	
CC	glycosylated. It can be used against dif	
CC	levels of either myeloid or lymphoid cel	
CC	It may also be used in conjunction with	
CC	as a hybridoma growth factor in culture	
CC	See also N80300.	
CC	Sequence 1139 BP.	361 A;
CC		240 C;

Query Match 35.1%; Score 565.2; DB 1; Length 1139;
Best Local Similarity 99.5%; Pred. No. 7.6e-136;
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1042	ccgataccccagagagaagattccaaagatgtagccgccccacacagacagcactcaacc	1101
Db	135	CCAGTAGCCCCAGAGAGAAATTCCAAAGATGATAGCGGCCCCACACAGACGCCACTCACC	194
Qy	1102	tcttcagaagaattgacaaacaaattcgttacatctcgacgcacatctcagccctgaga	1161
Db	195	TCCTTCAGAACGAATGACAAACAAATTTCGGTACATCTCTGACGGCGATCTCAGCCCTGAGA	254
Qy	1162	aaggagacatgtaacaagagtagtaacatggtgaaagcagcaaaagcagcactggcgagaaaac	1221
Db	255	AAGGAGACATGTAACAAGAGTAACATGTGTGAAAGCAGCAAAAGAGGCACCTGGCAGAAAAC	314
Qy	1222	aacctgaaccttcaagatggtctgaaaagatggatgtcttccaatctggtattcaatgag	1281
Db	315	AACCTGAACCTTCCTCAAGATGGCTGAAAAGATGGATGCTTCTCCAATCTGGATTCAATGAG	374
Qy	1282	gagactgcctgggtgaaaatacatcactcgtggtcttttgaggttgaggtatacctagatgac	1341
Db	375	GAGACTTGCCCTGGTGGAAATCATCACCTGGTCTTTTGGAGTTTGAGGTATACCTAGAGTAC	434

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QY 1342 ctccagaacagattgagtagtgaggaacaaagccagagctgtgcagatgagtacaaaa 1401
|||||
Db 435 CTCACAGACAGATTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAA 494
|||||
QY 1402 gtccgtatccagttcctcgcagaaaggaaggaatctagatgcaataaacaccctcgac 1461
|||||
Db 495 GTCCGTGATCCAGTTCTCAGAAAAAGCAAGAAATCTAGATGCAATAAACACCCTGAC 554
|||||
QY 1462 caaacacaaatgccagctctacgaagctgcagcacagaaacacagctgctcaggac 1521
|||||
Db 555 CGAACCAAAATGCCAGCTCTGACGAAGCTGCAGGCACAGAACCCAGTGGCTGCAGGAC 614
|||||
QY 1522 atgacaactcatctctcgtcgcagcttttaaggagttcctgcagtcagcctgagggct 1581
|||||
Db 615 ATGACAACATCATCTCTCGCAGCTTTTAAGGAGTTCTTGAGTCCAGCTCAGGCTGAGGCT 674
|||||
QY 1582 cttcgcaaatgtagcatggcgaccctgca 1611
|||||
Db 675 CTTCCGCAAAATGTAGCATGGCACCCTCAGA 704
|||||

RESULT 12
Q01763
ID Q01763 standard; DNA; 1162 BP.
AC Q01763;
DE 27-JUL-1990 (first entry)
KW BSF-2 gene for human B-cell differentiation factor.
OS Homo sapiens.
FH key Location/Qualifiers
FT cds 73..708
FT /*tag= a
FT cds J02009388-A.
PN 12-JAN-1990.
PD 8-JUL-1988; 170142.
PE 9-MAR-1988; JP-055270.
FA (AJIN) Ajinomoto KK.
DR WPI; 90-055348/08.
DR P-PSDB; R05415.
PT Physiologically active protein prep..
PT by transforming plasmid having gene coding physiologically
PT active protein and gene of di:hydrofolic acid reductase to hamster
PT ovary etc.
PS Example 3; Fig 6; 12pp; Japanese.
SC Gene may be expressed by transforming a dhfr negative strain of CHO cells
CC with an active BSF-2 gene and dhfr carrying vector. The BSF-2 gene is
CC a B-cell differentiating factor.
SQ Sequence 1162 BP; 359 A; 237 C; 264 G; 302 T;

Query Match 35.1%; Score 565.2; DB 1; Length 1162;
Best Local Similarity 99.5%; Pred. No. 7.6e-136;
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1042 ccagatccccagagagaattccaaagatgtagccgccccacacagacgacctacc 1101
|||||
Db 157 CCAGTACCCCCAGGAGAAGATTCCAAAGATGTAGCCGCCCCACACAGACGACCTCACC 216
|||||
QY 1102 tcttcagaacgaattgacaaataatcggtacatctcgtcagcgccatctcagccctgaga 1161
|||||
Db 217 TCTTCAGAACGAATTGACAAACAATTCGGTACATCTCTCGACGGCATCTCAGCCCTCAGA 276
|||||
QY 1162 aaggagacatgaaacagagtaacatgtgtgaaagcagcaaaagagcactggcagaac 1221
|||||
Db 277 AAGGAGACATGTACAGAGATTAACATGTGTCAAGCAGCAAAAGAGGACCTGGCAGAAAAC 336
|||||
QY 1222 aacctgaacctccaagatggctgaaagagatggatgcttccaatctggtattcaatgag 1281
|||||
Db 337 AACCTGAACCTTCCAAAGATGGCTGAAAGAGATGGATGCTTCCAAATCTGGATTCAATGAG 396
|||||
QY 1282 gagacttgctgtgaaataatcaatcactggtcttttggatttgaggttatcctagatc 1341
|||||
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Db 397 GAGACTTGCCTGGTGAAAAATCATCACTGGTCTTTTGGAGTTGAGGTATACCTAGAGTAC 456
|||||
QY 1342 ctccagaacagattgagtagtgaggaacaaagccagagctgtgcagatgagtacaaaa 1401
|||||
Db 457 CTCAGAACAGATTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAA 516
|||||
QY 1402 gtccgtatccagttcctcgcagaaaggaaggaatctagatgcaataaacaccctcgac 1461
|||||
Db 517 GTCTGTATCCAGTTCTCCTCAGAAAAAGCAAGAAATCTAGATGCAATAAACACCCTGAC 576
|||||
QY 1462 ccaaccacaaatgccagctcgtgcagaaagctgcagcacagaaacacagctgctcaggac 1521
|||||
Db 577 CCAACCAAAATGCCAGCTCTGACGAAGCTGCAGGCACAGAACCCAGTGGCTGCAGGAC 636
|||||
QY 1522 atgacaactcatctcgtcgcagcttttaaggagttcctgcagtcagcctgagggct 1581
|||||
Db 637 ATGACAACATCATCTCTGCGCAGCTTTTAAGGAGTTCTTGAGTCCAGCTCAGGCTGAGGCT 696
|||||
QY 1582 cttcgcaaatgtagcatggcgaccctgca 1611
|||||
Db 697 CTTCCGCAAAATGTAGCATGGCACCCTCAGA 726
|||||

RESULT 13
N90131
ID N90131 standard; DNA; 1101 BP.
AC N90131;
DE 1-NOV-1989 (first entry)
KW BSF2-L8; pGEM4; cDNA; clone; Fc epsilon R-gene; IgE; allergy.
FH key Location/Qualifiers
FT misc_feature 1..6
FT /*tag= a
FT cds 7..642
FT /*tag= b
FT misc_feature 1097..1101
FT /*tag= c
FT EP-321842-A.
PN 28-JUN-1989.
PD 14-DEC-1988; 120878.
PE 22-DEC-1987; EP-100814.
FA (OSAU) Osaka University.
PR Kishimoto T, Suekura M, Kikutani H, Barsumian EL, Schneider FJ;
PI WPI; 89-186249/26.
DR P-PSDB; P90047.
DR Cloned gene for eukaryotic expression of Fc epsilon receptor
PT - for use in treatment and prophylaxis of allergy, esp. asthma.
PS Disclosure; fig 3; 24pp; English.
CC BSF2-L8 is prepd. by digesting pBSF-2.38 with HindIII and BamHI
CC to obtain a 1.2 kbp EcoRI-BamHI BSF-2 cDNA insert. This was digested
CC with HinfI, end-filled, and and digested with KpnI. A 100 bp
CC KpnI-HinfI fragment contg. BSF-2 leader sequence was cloned into
CC the multiple cloning site of KpnI-SmaI digested pGEM4, and one of the
CC selected clones named as pBSF2-L8. It is used in prepn. of pSFC
CC epsilon R-1 (see N90132). The misc. feature a is a KpnI site, and
CC c is a BamHI site. The encoded peptide sequence (see P90047) includes
CC that of the BSF-2 signal sequence.
SQ Sequence 1101 BP; 351 A; 227 C; 224 G; 299 T;

Query Match 35.0%; Score 563.6; DB 1; Length 1101;
Best Local Similarity 99.3%; Pred. No. 1.9e-135;
Matches 566; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1042 ccagatccccagagagaattccaaagatgtagccgccccacacagacgacctacc 1101
|||||
Db 91 CCAGTACCCCCAGGAGAAGATTCCAAAGATGTAGCCGCCCCACACAGACGACCTCACC 150
|||||
QY 1102 tcttcagaacgaattgacaaataatcggtacatctcgtcagcgccatctcagccctgaga 1161
|||||
Db 151 TCTTCAGAACGAATTGACAAACAATTCGGTACATCTCTCGACGGCATCTCAGCCCTCAGA 210
|||||
QY 1162 aaggagacatgtaacaagagtaacatgtgtgaaagcagcaaaagagcactggcagaac 1221
|||||
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Db 211 AAGGAGACATGTAAAGAGTAACATGTGTGAAGCAGCAAGAGGCACTGGCAGAAAAC 270
QY 1222 aacctgaacctccaaagatgctaaaaagatgagcttcccaatctggattcaatgag 1281
Db 271 AACCTGAACCTTCCAAAGATGCTGAAAAGATGGATGCTTCCAACTCGGATTCATGAG 330
QY 1282 gagacttgctgggtgaaatacatcactggtctctttggagtttgaggtatatacctagatgac 1341
Db 331 GAGACTTGCTGGTGAATAATCATCACTGGTCTTTTGGAGTTTGAGGTATACCTAGAGTAC 390
QY 1342 ctccagaacagattgagtagtgaggaacaagccagagctgtgcagatgagtagtaaaaa 1401
Db 391 CTCCAGAAACAGATTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAAA 450
QY 1402 gtccctgatccagttctcagaaaaagcagaagaatctagatgcataaaccacctgac 1461
Db 451 GTCCCTGATCCAGTTCCTCGAAAAAGGCAAGAATCTAGATGCAATTAACCAACCCCTGAC 510
QY 1462 ccaaccacaaatgccagctgctgacgaagctgcaggcagacaaaccagtggctgcaggac 1521
Db 511 CCAACCAAAATGCCAGCTGCTGACGAAGCTGCAGGCACACAGACCACTGGCTGCAGGAC 570
QY 1522 atgacaactatctctctgcagcagcttttaaggagttctctgcagctcagcagctgagggct 1581
Db 571 ATGACAACCTCATCTCATTTCTGGCAGCTTTAAGGAGTCTCTGCAGTTCAGCCTGAGGGCT 630
QY 1582 ctccggcaaatgtagcatgggcacccgtcga 1611
Db 631 CTTCGGCAAAATGTAGCATGGGCACCTCAGA 660

RESULT 14
N90135
ID N90135 standard; DNA; 1101 BP.
AC N90135;
DE 1-NOV-1989 (first entry)
KW DNA sequence of pBSF2-L8
FH Key Location/Qualifiers
FT misc_feature 2..5
FT cds /*tag= a
FT /*tag= b
FT /*tag= c
PN EP-321601-A.
PD 28-JUN-1989.
PF 22-DEC-1987; 119080.
PR 22-DEC-1987; EP-119080.
PA (OSAU) Osaka University
PI Kishimoto T, Suemura M, Kikutani H, Barsumian E;
DR WPI: 89-186101/26.
DR P-PSDB; P90371.
PT Cloned genes coding for soluble IgE receptor - comprising modified coding
sequence of Fc epsilon receptor gene.
PS Disclosure: fig. 3; 20pp; English.
CC Sequence of pBSF2-L8, which is used as a vector in prepn. of plasmid
pSfc epsilon R-1. It is prepd. by inserting BSF-2 cDNA insert (from
pBSF-2.38) into pGEM4. Misc. feature a is a KpnI site, and c is a BamHI
site. See also N90134, N90136 and P90371 for encoded peptide.
SQ Sequence 1101 BP; 351 A; 227 C; 224 G; 299 T;

Query Match 35.0%; Score 563.6; DB 1; Length 1101;
Best Local Similarity 99.3%; Pred. No. 1.9e-135;
Matches 566; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1042 ccagtaccctccagagagattccaaagatagcgcgcccaacacagacagaccactacc 1101
Db 91 CCAAGTACCCCGAGGAGAGATTCCAAAGATGTAGCCGCCGCCACACAGACAGCACTCACC 150
QY 1102 tcttcagaacgaattgacaaacaattcggtacatctctcgacggcgtatctcagccctgaga 1161

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Db 151 TCTTCAGAAGCAATTCACAAACAAATTCGCTACATCTCGAGCGCATCTCAGCCCTGAGA 210
QY 1162 aaggagacatgtatacaagagtgtaacatgtgtgaaagcagcaagagaggaactggcagaaaa 1221
Db 211 AAGGAGACATGTAAAGAGTAGTAACATGTGTGAAGCAGCAAGAGGCACTGGCAGAAAAC 270
QY 1222 aacctgaacctccaaagatgctgaaagaagatggatgcttcccaatctggattcaatgag 1281
Db 271 AACCTGAACCTTCCAAAGATGCTGAAAAGATGGATGCTTCCAACTCGGATTCATGAG 330
QY 1282 gagacttgctgggtgaaatacatcactggtctctttggagtttgaggtatatacctagatgac 1341
Db 331 GAGACTTGCTGGTGAATAATCATCACTGGTCTTTTGGAGTTTGAGGTATACCTAGAGTAC 390
QY 1342 ctccagaacagattgagtagtgaggaacaagccagagctgtgcagatgagtagtaaaaa 1401
Db 391 CTCCAGAAACAGATTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAAA 450
QY 1402 gtccctgatccagttctcagaaaaagcagaagaatctagatgcataaaccacctgac 1461
Db 451 GTCCCTGATCCAGTTCCTCGAAAAAGGCAAGAATCTAGATGCAATTAACCAACCCCTGAC 510
QY 1462 ccaaccacaaatgccagctgctgacgaagctgcaggcagacaaaccagtggctgcaggac 1521
Db 511 CCAACCAAAATGCCAGCTGCTGACGAAGCTGCAGGCACACAGACCACTGGCTGCAGGAC 570
QY 1522 atgacaactatctctctgcagcagcttttaaggagttctctgcagctcagcagctgagggct 1581
Db 571 ATGACAACCTCATCTCATTTCTGGCAGCTTTAAGGAGTCTCTGCAGTTCAGCCTGAGGGCT 630
QY 1582 ctccggcaaatgtagcatgggcacccgtcga 1611
Db 631 CTTCGGCAAAATGTAGCATGGGCACCTCAGA 660

RESULT 15
N90345
ID N90345 standard; DNA; 1101 BP.
AC N90345;
DE 1-NOV-1989 (first entry)
KW Plasmid pBSF2-L8, encoding whole human lymphocyte receptor
FH Key Location/Qualifiers
FT cds /*tag= a
FT /*tag= a
PN EP-324879-A.
PD 26-JUL-1989.
PF 20-JAN-1988; 100814.
PR 20-JAN-1988; EP-100814.
PA (KISH) Kishimoto T.
PI Schwendenwein R, Sommergruber W, Swetly P;
DR WPI: 89-214148/30.
DR P-PSDB; P90121.
PT Soluble recombinant Fc-epsilon receptor
PT - used for treatment or prophylaxis of local and
allergic reactions induced by IgE.
PS Disclosure: fig 3; 24pp; English.
CC Plasmid pBSF2-L8, encoding whole human lymphocyte receptor
for immunoglobulin (see P90121). Has BSF-2 leader sequence
(c.f. N90344). Used to produce highly bioactive
CC water-soluble FcR. Pref. has interleukin signal sequence.
CC Water-soluble FcR binds IgE, so it is useful for treating
CC hypersensitivity, esp. asthma.
SQ Sequence 1101 BP; 351 A; 227 C; 224 G; 299 T;

Query Match 35.0%; Score 563.6; DB 1; Length 1101;
Best Local Similarity 99.3%; Pred. No. 1.9e-135;

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Matches 566; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1042 ccagttaccctccaggagagattccaaagatgtagccgccccacacagacagccactcacc 1101
Db 91 CCAGTACCCCCAGGAGAGATTCCAAAGATGTAGCCGCCCCACACAGACGCCACTCACC 150

Qy 1102 tcttcagaaacgaattgacaaacaaattcgtgtacatcctcgcagcgcacatcagccctgaga 1161
Db 151 TCTTCAGAACGAATTGACAAACAAATTCGGTACATCCTCGACGGCATCTCAGCCCTGAGA 210

Qy 1162 aagagacatgtaacaagagtaaacatgtgtgaaagcagcaaaagagcactggcagaaaaac 1221
Db 211 AAGGAGACATGTAAACAGAGTAACATGTGTGAAAGCAGCAAAAGAGGCACCTGGCAGAAAAAC 270

Qy 1222 aacctgaaccttccaaagatggtgaaaaagatggtatgcttccaaatctggaattcaatgag 1281
Db 271 AACCTGAACCTTCCAAAGATGGCTGAAAAGATGGATGCTTCCAAATCTGGATTCAATGAG 330

Qy 1282 gagacttgcttggtgaaaaatcatcactggtcttttggagtttgaggtatacctagagtac 1341
Db 331 GAGACTTGCTTGGTGAATAATCATCTGGTCTTTTGGAGTTTGAGGTATACCTAGAGTAC 390

Qy 1342 ctccagaaacagatttgagagtagtgaggaaacacccagagctgtgcagatgagtacaaaa 1401
Db 391 CTCCAGAAACAGATTGAGAGTAGTGAGGACACAGCCAGAGCTGTGCAGATGAGTACAAAA 450

Qy 1402 gtcctgatccagttcctgcagaaaaagcaaaagatctagatgcaataaacacccctgac 1461
Db 451 GTCCTGATCCAGTTCCCTGCAGAAAAGGCAAAAGAAATCTAGATGCAATAACCCCCCTGAC 510

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Db 571 ATGACAACCTCATCTCTCTCCGAGCCTTTAAGGAGTTCCTGACAGTTCCAGCCTGAGGGCT 630

Qy 1582 cttcggcaaatgtagcatgggcacgcgcga 1611
Db 631 CTTGGCAAAATGTAGCATGGGCACCTCAGA 660

Search completed: August 9, 2000, 09:34:47
Job time: 34153 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 9, 2000, 07:00:26 ; Search time 2865.12 Seconds
(without alignments)
1004.122 Million cell updates/sec

Title: US-09-142-471-3

Perfect score: 1612

Sequence: 1 gtcacgcacgtgagtgtag.....gtacatgggcacogtcgac 1612

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 972840 seqs, 892348106 residues

Total number of hits satisfying chosen parameters: 1945680

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba1:*

2: gb_ba2:*

3: gb_om:*

4: gb_ov:*

5: gb_pat:*

6: gb_ph:*

7: gb_pl1:*

8: gb_pl2:*

9: gb_pr1:*

10: gb_pr2:*

11: gb_pr3:*

12: gb_ro:*

13: gb_sts:*

14: gb_sy:*

15: gb_un:*

16: em_fun:*

17: em_hum1:*

18: em_hum2:*

19: em_in:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_sy:*

29: em_un:*

30: em_vi:*

31: gb_htg1:*

32: gb_htg2:*

33: gb_in1:*

34: gb_in2:*

35: em_ba1:*

36: em_ba2:*

37: em_hum3:*

38: em_hum4:*

39: gb_pr4:*

40: gb_htg3:*

41: gb_htg4:*

42: gb_htg5:*

43: gb_htg6:*

44: gb_htg7:*

45: em_htg1:*

46: em_htg2:*

47: em_htg3:*

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54: gb_htg11:*

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63: em_htg5:*

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65: em_htg7:*

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72: gb_htg23:*

73: gb_htg24:*

74: gb_htg25:*

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76: gb_htg27:*

77: gb_htg28:*

78: gb_htg29:*

79: gb_htg30:*

80: gb_htg31:*

81: gb_vil:*

82: gb_v12:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1612	100.0	1612	5	A93715	A93715 Sequence 2
2	1587	98.4	1627	5	A93714	A93714 Sequence 1
3	995	61.7	2056	5	E04823	E04823 CDNA encod1
4	995	61.7	2087	5	E02673	E02673 CDNA encod1
5	995	61.7	3319	5	E12979	E12979 CDNA encod1
6	995	61.7	3319	9	HSIL6R	X12830 Human mRNA
7	993.4	61.6	1486	9	HSIGREC	X58298 Human mRNA
8	969	60.1	1074	5	AR031384	AR031384 Sequence
C 9	581	36.0	167677	69	AC013588	AC013588 Homo sapi
C 10	581	36.0	175587	59	AC015889	AC015889 Homo sapi
C 11	577.8	35.8	168014	40	AL353649	AL353649 Homo sapi
C 12	577.8	35.8	168372	40	AL161629	AL161629 Homo sapi
13	565.2	35.1	1098	9	HSILB2R	X04602 Human mRNA
14	565.2	35.1	1102	5	E03737	E03737 CDNA encod1
15	565.2	35.1	1102	10	HUMIL6C	M29150 Human inter
16	565.2	35.1	1113	11	HUMIL6CSF	M54894 Human inter
17	565.2	35.1	1125	9	HUMIFNB2B	M18403 Human hybri
18	565.2	35.1	1139	5	I08633	I08633 Sequence 2
19	565.2	35.1	1161	5	E01616	E01616 CDNA encod1
20	565.2	35.1	1162	5	E01518	E01518 DNA encodin
21	565.2	35.1	1162	5	E01537	E01537 DNA encodin
22	565.2	35.1	1162	5	E02030	E02030 CDNA sequen
23	565.2	35.1	1162	5	E02202	E02202 DNA encodin
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RESULT 4
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LOCUS CDNA encoding human B cell stimulating factor 2 receptor protein.
DEFINITION E02673
ACCESSION E02673
VERSION E02673.1 GI:2170901
KEYWORDS JP 1990288898-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
TITLE Primates; Catarrhini; Hominiidae; Homo.
JOURNAL Kishimoto, C.
HUMAN B CELL STIMULATION FACTOR 2 RECEPTOR PROTEIN
Patent: JP 1990288898-A 1 28-NOV-1990;
KISHIMOTO CHUZO
COMMENT OS Homo sapiens (human)
PN JP 1990288898-A/1
PD 28-NOV-1990
PF 20-JAN-1989 JP 1989009774
PR 22-JAN-1988 JP 88P 12387, 25-JAN-1988 JP 88P 12599, PR
04-AUG-1988 JP 88P 194885, 14-JAN-1989 JP 89P 7461 PI
KISHIMOTO CHUZO
PC C07K15/06, C07K13/00, C12N5/10, C12N5/20, C12N15/19, C12N15/85, PC
C12P21/02,
PC C12P21/08//A61K37/02, A61K37/02, A61K39/395, C12N15/06,
PC C12P21/02,
PC C12R1.91), (C12P21/08, C12R1.91);
CC strandedness: Doublet;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: cell_type=natural killer cell;
CC *source: cell_line-YT;
CC *source: clone-piBBSF2R;
FH Key Location/Qualifiers
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FT /product="human B cell stimulating factor 2
FT receptor
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FT mat_peptide 313..1650
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FT 1..2087
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BASE COUNT 425 a 645 c 623 g 394 t
ORIGIN

Query Match 61.7%; Score 995; DB 5; Length 2087;
Best Local Similarity 100.0%; Pred. No. 2.3e-229;
Matches 995; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 68 tgctggccgcgcggagcgcgctggcccccagagcgctgcccctgacgagagtgga 127
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QY 128 gagcgctgctgaccagctctgccaggagacagcgtgactctgacactgccccggggtagagc 187
Db 341 GAGCGCTGCTGACCACTCTGCCAGGACAGCGTGACTCTGACCTGCCCGCGGGGTAGAGC 400
QY 188 cgaagacaatgccactgttcaactgggtgctcaggaagcggctgagggctccaccccc 247
Db 401 CGGAAGACAATGCCACTGTTCACCTGGGTGCTCAGGAAGCGGCTGCAAGGCTCCACCCCA 460
QY 248 gcagatggcgctggcagtggaagagcgctgctgctgaggtcggtgacgtccacagactcg 307
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QY 308 gaaactattcatgctaccggggcgcccgccagctgggactgtgcaactgtctggtggtg 367
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QY 488 agttcagaacagtcgccggcggaagacttccaggagcgctgcccagtgattccacagagtc 547
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RESULT 5
E12979
LOCUS CDNA encoding human interleukin-6 receptor.
DEFINITION E12979
ACCESSION E12979
VERSION E12979.1 GI:3251803
KEYWORDS JP 1997118623-A/1.
SOURCE Homo sapiens.

JOURNAL MEDLINE FEATURES source	Science 241 (4867), 825-828 (1988) 88305347 Location/Qualifiers 1. .3319 /organism="Homo sapiens" /db_xref="taxon:9606" /cell_line="YF" /clone="pBSF2R.236" 438. .494 /product="signal peptide (AA -19 to -1)" 438. .1844 /codon_start=1 /product="IL-6 receptor precursor (AA -19 to 449)" /protein_id="CAA31312.1" /db_xref="GI:33846" /db_xref="SWISS-PROT:P08887" /translation="MLAVGALLAALLAAPRCAPQAEVARGVLTSLPDSVT LTCGPVEDNATVHVLKPAAGSHPSRWAGMRLLRLRSVOLHDSGNYSCYRAGR AGTVHLVDVPEEPQLSCFRKPSLSNVVCEWGPSTPSLTAKVLLVLRKFNQSPAD FQPCQYQSQESKQLAVPEGDSFYIVSMCVASSVSGSKFTQTQFGCGILQDPD PANITVAVARNPRLSVTWQDPHSHNSFYRLRFLRYRAERSKFTTVMVKDLQHH CVTHDWSGLRHVOLRAOEFGOGSEWSPAMGTPWTERSPAEVSTPMOAL TNKDDNLIIFRDSANATSLPVDSSVPLPFLVAGSLAGTLLCIAIVLRFKKTW KLRLREGTSNHPPTSLGOLVPRPRPTVPLVPLSPVPSLSLGSNDTSSNRPDA RDRSPYDISNTDYFPPR" 495. .1841 /product="IL-6 receptor (AA 1-449)" 495. .764 /note="Ig superfamily domain" 600. .608 /note="pot. N-linked glycosylation site" 714. .722 /note="pot. N-linked glycosylation site" 1098. .1106 /note="pot. N-linked glycosylation site" 1170. .1178 /note="pot. N-linked glycosylation site" 1485. .1493 /note="pot. N-linked glycosylation site" 1512. .1595 /note="transmembrane domain" 1758. .1766 /note="pot. N-linked glycosylation site" 3134. .3139 /note="pot. polyA signal" 3159. .3164 /note="pot.alt. polyA signal" 3319 /note="polyA site"	mat_peptide misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature polyA_site	248 652 308 712 368 772 428 832 488 892 548 952 608 1012 568 1072 728 1132 788 1192 848 1252 908 1312 968 1372	gcagatgggctggcaggaaggaggtgctgctgagtgctgagtcagctccacgactctg GCAGATGGGCTGGCATGGGAAGGAGGCTGCTGCTGAGTGGTCCAGCTCCACGACTCG gaaactattcatgctaccgggcccggcccagctggagactgtgcacttgcgtggtgatg GAAACTATTGCTACCGGCGCGGCCGCCAGCTGAGTGGACTGTGCACCTTGTGTGGATG ttccccccgaggagcccgactctcttgcctccggaagagcccccctcagcaaatgtgtt TTCCCCCGGAGGAGCCCGACGCTCTCTGCTTCCGGAAGAGCCCCCTCAGCAATGTGT gtagtggtggctctcggagcaccctccctgcagcaaaaagctgtgtctcttctgtgagga GTGAGTGGGTCCTTCGGAGCACCCTCCCTTGACACAAAGGCTGTGCTCTTGTGTGAGGA agtttcagaacagtcctcggcgaagactctccaggagcgcgtgccagtattcccagagtcctc AGTTTTCAGAACAGTCCGCGCGCAAGACTTCCAGGAGCGGTGCCAGTATTCCCGAGGAGTCCC agaagtctcctgcagtagcagtcctcggagcagcagcagcagcagcagcagcagcagcagc AGAAAGTTCTCTGCGAGTGTAGCTCCGCGAGGAGGAGAGCTCTTTTACATAGTGTCCTCA tgtgctgcgcagctagtgctcgggagcaggttcagcaaaactcaaacctttcaggggtgtg TGTGCGTGGCCAGTGTGTCGGGAGCAAGTTTCAGCAAAACTCAAACTTTTCAGGGTTGTG gaatttcgagcctgctcgcctcgcctcgcctcgcctcgcctcgcctcgcctcgcctcgcctc GAATCTTTCAGGCTGATCCGCTGCCAACATCACAGTCACTGCGGTGGCCAGAAACCCCC gctggtcagtgctcactgtgcaagaccccccaactcctcgaactcattcttctacagactac GCTGGCTCAGTGTCACTGGCAAGACCCCCCACTCTGGAATCACTTTTCTACAGACTAC ggttgagctcagatcgggctgcaagcgggtcaagagcattcacacatggatgggtcgaagg GGTTGAGCTCAGATATCGGGCTCAACGGTCAAGAGACTTTCACAACTGGATGTCGCAAGG acctccagcactcagtgctcctccacgacgcctggagcgcctggagcagcagcagcagcagc ACCTCCAGCATCACTGTGTATCCAGCAGCGCTGAGCGGCTGAGGCACCTGGTGCAGC ttcgtgccagaggagaggttcgggcaagcagcagcagcagcagcagcagcagcagcagcagc TTCTGTCCCGAGGAGGAGTTCGGGCAAGCGGAGTGGAGTGGAGCCCGGAGGCCCATGG gcacgcttgagacaagaatccaggagtcctccagct GCAGGCTTGGACAGAAATCCAGGAGTCTCTCCAGCT	307 711 367 771 427 831 487 891 547 951 607 1011 667 1071 727 1131 787 1191 847 1251 907 1311 967 1371 1002 1406	RESULT 7 HS16REC LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE	Human mRNA for interleukin-6-receptor. X58298 X58298.1 GI:32580 cell surface receptor; Interleukin 6 receptor. human. Homo sapiens Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. Schooltink, H. Direct Submission. Submitted (12-MAR-1991) H. Schooltink, Dept of Biochemistry, RWTH Aachen Klinikum, Pauwelsstrasse 30, 5100 Aachen, Germany 2 (bases 1 to 1486) Schooltink, H., Stoyan, T., Lenz, D., Schmitz, H., Hirano, T., Kishimoto, T., Heinrich, P.C. and Rose-John, S. Structural and functional studies on the human hepatic
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QY 94 gccccaggcgctgcccctgcgcaggaggtggcgaagagcgctgtgaccagctgtgccagga 153
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RESULT 9
LOCUS AC013588/c
DEFINITION Homo sapiens clone RP11-8B23, WORKING DRAFT SEQUENCE, 15 unordered
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ACCESSION AC013588
VERSION AC013588.3 GI:7329375
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
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SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 167677)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens, clone RP11-8B23

Unpublished

2 (bases 1 to 167677)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,B., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgaiter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collamore,A.,
Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galaan,J., Gardyna,S., Grant,G., Hagos,B., Harford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lechoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Rhomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 26, 2000 this sequence version replaced gi:6514000.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L2963

Center clone name: 8.B.23

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 159183 bases at least Q40

Consensus quality: 163476 bases at least Q30

Consensus quality: 164920 bases at least Q20

Insert size: 165000; agarose-fp

Insert size: 166277; sum-of-contigs

Quality coverage: 4.2 in Q20 bases; agarose-fp

Quality coverage: 4.2 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 15 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 2090: contig of 2090 bp in length

* 2091 2190: gap of 100 bp

* 2191 4992: contig of 2802 bp in length

* 4993 5092: gap of 100 bp

* 5093 7384: contig of 2292 bp in length

* 7385 7484: gap of 100 bp

* 7485 11034: contig of 3550 bp in length

* 11035 11134: gap of 100 bp

* 11135 15041: contig of 3907 bp in length

* 15042 15141: gap of 100 bp

* 15142 21265: contig of 6124 bp in length

* 21266 21365: gap of 100 bp

* 21366 28896: contig of 7531 bp in length

* 28897 28996: gap of 100 bp

* 28997 34811: contig of 5815 bp in length

JOURNAL
REFERENCE
AUTHORS

Unpublished
2 (bases 1 to 175587)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Headford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

TITLE
JOURNAL
COMMENT

Direct Submission
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 28, 2000 this sequence version replaced gi:6563517.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information

Center project name: L752
Center clone name: 251_E_22
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 154641 bases at least Q40
Consensus quality: 167036 bases at least Q30
Consensus quality: 172180 bases at least Q20
Insert size: 190000; agarose-fp
Insert size: 175087; sum-of-contigs
Quality coverage: 5.0 in Q20 bases; agarose-fp
Quality coverage: 5.0 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1043: contig of 1043 bp in length
* 1044 1143: gap of 100 bp
* 1144 2746: contig of 1603 bp in length
* 2747 2846: gap of 100 bp
* 2847 4016: contig of 1170 bp in length
* 4017 4116: gap of 100 bp
* 4117 5741: contig of 1625 bp in length
* 5742 5841: gap of 100 bp
* 5842 88987: contig of 83146 bp in length
* 88988 89087: gap of 100 bp
* 89088 175587: contig of 86500 bp in length.

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/db_xref="taxon:9606"
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/map="17"
/clone="RP11-251E22"
/clone_lib="RPC1-11 Human Male BAC"
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/note="assembly_fragment"
1144..2746

misc_feature

misc_feature

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	misc_feature	vector_side:left"	
BASE COUNT	47814 a	38265 c	39394 g
ORIGIN		501 others	

Query Match	36.0%;	Score 581;	DB 59;	Length 175587;
Best Local Similarity	77.9%;	Pred. No. 1.5e-129;		
Matches	775;	Conservative 0;	Mismatches 190;	Indels 30; Gaps 5;

QY	8	catggagtggtagccagaggaagcatgctggccctggctggctgagctgagctgagctgccc	67
Db	85419	CATGGGCAATTAGCCAAAGGAAGGATGCTGGCCATCAGCTGAGTGTCTGTGGCCACAC	85360
QY	68	tgtgtgcccgcgcgggagcgctggtgccccagggcgctgccccagggaggtggcaca	127
Db	85359	TGCGGGCAGTGTCTGGG-----CCCAAGAGGCTGCCCTACGCTGGAGGAGGAGAAC	85313
QY	128	gaggcgctgtgaccagctgtccaggagacagcgctgactctgacctgacccgggggtagagc	187
Db	85312	GTGATGTGTGA-----CCAGGATATGTCATTCCTTGCAGCTGTCCAGAGGAGGAGAAC	85261
QY	188	cggaaacaaatgccactgttcactgggtgctcaaggagcggcgctgaggtcccccaca	247
Db	85260	CTGAAATCATGCTGCCTGCTGCTGTCACAGGACTCCACAGCGAGGCTCAGGCCCA	85201
QY	248	gcagatggcgctgcatgggaaggagcgctgctgctgaggtcggtgagctccacgactctg	307
Db	85200	GCAGATGGGCTGGTGGGAGGAGGCTGCTTCTGAGTTGGTGCAGCTTCGCAGCTCTG	85141
QY	308	gaactattcatgctaccggcgccgcccagctgggactgtgacctgtgctgtggtgagtg	367
Db	85140	GAAACTATTCTGCTGCCGGCTGGCTGCCACAGG--TCTGTGCTTTTGTGTGTGATG	85083
QY	368	ttccccccaggagccccagctctctgtctccgggaagagccccctcagcaatgtgttt	427
Db	85082	TTTCTCTGAGGAGCCTCAGCTCTCTGCTTCTGGAAGAGAGCCCCCTCAGTGCATTTGTT	85023
QY	428	gtgagtgggtgctctcgagaccccccatccctgacgacaaaggctgtgctcttggtagga	487
Db	85022	GTGAATAGAGTCTCTGGAGTCAAGGTTCTGAGTC----AAAGCTGTCTATTGGTGA	84967
QY	488	agttcagaacagctccggccgaagacttccaggagccgtgccagatttccaggagtgccc	547
Db	84966	AGTTTCAGAACTGTACGGCAGAACTCTTCCAGGAGCGGTGCAGTATTCTCAGGAGTCCC	84907
QY	548	agaagtctctccagtttagcagtcctccggagggagacagctcttttctacatagtgcca	607
Db	84906	AGAAGTT---CTGCCAGTTGGCAGTGCACAGAGGAGATTACTCTTCTATACAGTGTCCC	84850
QY	608	tgtgcgtcgccagtagtgcgggagcaagtccagcaaaactcaaacctttcagggttggtg	667
Db	84849	TGTGTGTCAACACAGTATTGGGAGCAAGTTTCAGCAAAACCAAAATATTAGAGGTTATG	84790
QY	668	gaacttcgagcctgatccgctgcccaacatcacagtcactgcggtggccagaaaccccc	727
Db	84789	GAATCTGTCAGTCCGACCCACCTGTCAACATCACAGTCATTGTGTGTGGCCAGAAAGCCCT	84730
QY	728	gctggtcagtgctcaactggcagaagcccccaactccttggaactcatctttctacagctac	787
Db	84729	GCTGGCTCAACGTCACCTAGCAAGACCCCACTCTCTGGAACCTTATATTTCTACAGCTAT	84670

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QY 788 gggttgagctcagatcggtggaacggtcaaacgattcaaacatggtggtcaagg 847
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 84669 GGTtTGAGCTTTGATACCTGGCTAAATAGTCAAAAATGTTTCATACATGATGGCCAAAG 84610
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 848 acctcagatcactgtgtcattccacagcgcctgagcgccctgagggcagctggtgcagc 907
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 84609 ATTCACCAATCATGCTGTCTCATTCACAAACACCTGGAAAGGCATGAGCCACACAGCAGC 84550
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QY 908 ttctgtccagagagaggttcgagcgaaggcagtgagcagtgagcagccgagggccatgg 967
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Db 84549 TTCAGCCCCAGAGGAGCTGGGGCAGAGCTTGTGAAGTGGAGCCAGAGGTCATGG 84490
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QY 968 gcacgccttggacagaatccaggagtcctccagct 1002
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Db 84489 GAACCTTTGGGAGACTCCAGGAGTCTCCAGCT 84455
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RESULT 11
AL353649/c
LOCUS
DEFINITION
AL353649 Homo sapiens chromosome 9 clone RP11-30P16, HTG 20-APR-2000
PROGRESS ***, in unordered pieces.
ACCESSION
AL353649
VERSION
AL353649.1 GI:7635196
KEYWORDS
HTG; HTGS_PHASE1.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (Bases 1 to 168014)
Plumb,B.
Direct Submission
Submitted (20-APR-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA30P16
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 153632 bases at least Q40
Consensus quality: 158903 bases at least Q30
Consensus quality: 162319 bases at least Q20
Insert size: 165814; sum-of-contigs
Insert size: 156868; agarose-fp
Quality coverage: 3.85x in Q20 bases; sum-of-contigs Quality
coverage: 4.07x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'unfinished' sequence. It currently * consists of
23 contigs. The true order of the pieces is * not known and their
order in this sequence record is * arbitrary. Where the contigs
adjacent to the vector can * be identified, they are labelled with
'clone_end' in the * feature table. Some order and orientation
information * can tentatively be deduced from paired sequencing
reads * which have been identified to span the gap between two
contigs. These are labelled as part of the same *
'fragment_chain', and the order and relative orientation * of the
pieces within a fragment_chain is reflected in * this file. Gaps
between the contigs are represented as * runs of N, but the exact
sizes of the gaps are unknown. * This record will be updated with
the finished sequence as * soon as it is available and the
accession number will be * preserved.
1 14912 contig of 14912 bp in length; fragment_chain 1
* 15013 17004 contig of 1992 bp in length; fragment_chain 1 *
17105 33287 contig of 16183 bp in length; fragment_chain 1 *
33388 38481 contig of 5094 bp in length; fragment_chain 1 *
38582 44792 contig of 6211 bp in length; fragment_chain 1 *

```

```

44893 47024 contig of 2132 bp in length; fragment_chain 2 *
47125 58864 contig of 11740 bp in length; fragment_chain 2 *
58965 60033 contig of 1069 bp in length
60134 61190 contig of 1057 bp in length
61291 69752 contig of 8462 bp in length
69853 70859 contig of 1007 bp in length
70960 72257 contig of 1298 bp in length
72358 73398 contig of 1041 bp in length
73499 74668 contig of 1170 bp in length
74769 82676 contig of 7908 bp in length
82777 101516 contig of 18740 bp in length
101617 102936 contig of 1320 bp in length
103037 114706 contig of 11670 bp in length
114807 115872 contig of 1066 bp in length
115973 117049 contig of 1077 bp in length
117150 136261 contig of 19112 bp in length
136362 160914 contig of 24553 bp in length
161015 168014 contig of 7000 bp in length.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
FEATURES
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Location/Qualifiers
1..168014
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/clone="RP11-30P16"
/clone_lib="RPC1-11.1"
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fragment_chain:1
clone_end:SP6
vector_side:left
15013..17004
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17105..33287
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33388..38481
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fragment_chain:1
38582..44792
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44893..47024
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*	40319	52258:	contig of 11940 bp in length	
*	52539	53058:	gap of	800 bp
*	53059	56394:	contig of 3326 bp in length	
*	56385	57184:	gap of	800 bp
*	57185	92891:	contig of 35707 bp in length	
*	92892	93691:	gap of	800 bp
*	93692	97942:	contig of 4251 bp in length	
*	97943	98742:	gap of	800 bp
*	98743	116105:	contig of 17363 bp in length	
*	116106	116905:	gap of	800 bp
*	116906	119375:	contig of 2470 bp in length	
*	119376	120175:	gap of	800 bp
*	120176	134110:	contig of 13935 bp in length	
*	134111	134910:	gap of	800 bp
*	134911	146286:	contig of 11376 bp in length	
*	146287	147086:	gap of	800 bp
*	147087	163093:	contig of 16007 bp in length	
*	163094	163893:	gap of	800 bp
*	163894	168372:	contig of 4479 bp in length.	

[illegible]

RESULT 13

HSILB2R	HSILB2R	1098 bp	mRNA	PRI	21-MAR-1995
LOCUS	Human mRNA for interleukin BSF-2 (B-cell differentiation factor)				
DEFINITION	X04602				
ACCESSION	X04602.1				
VERSION	GI:33849				
KEYWORDS	B-cell differentiation factor; interleukin BSF-2; signal peptide				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;				
	Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 1098)				
AUTHORS	Hirano, T., Yasukawa, K., Harada, H., Taga, T., Watanabe, Y., Matsuda, T., Kashiwamura, S.I., Nakajima, K., Koyama, K., Iwamatsu, A., Tsuchisawa, S., Sakiyama, F., Matsui, H., Takahara, Y., Taniguchi, T., Tsunashima, T., Kishimoto, T.				

FEATURES MEDLINE 87063033
Location/Qualifiers
 1. 1098
 source

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34. .117
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/product="put. signal peptide (AA -28 to -1)"
34. .672
CDS
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/note="pot. N-glycosylation site"
misc_feature 1072..1077
/note="put. polyA signal"
polyA_site 1098
/note="polyA site"
BASE COUNT 333 a 237 c 226 g 302 t
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Best Local Similarity 99.5%; Pred. No. 7.8e-126;
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1042 cagtagtccccaggagaagattccaaagatgtagccgccccacacagacagcactcacc 1101
DB 118 CCAGTACCCCGAGGAGAAATTCCAAAGATGTAGCGCGCCACACAGACAGCCACTCACC 177
QY 1102 tcttcagaacgaattgacaaaataatcggtacatctctcgacggcatctcagccctgaga 1161
DB 178 TCTTCAGAACGAATTGACAAACAAATTCGGTACATCTCGACGGCATCTCAGCCCTGAGA 237
QY 1162 aaggagacatgtaaacagatgaacatgtgtgaagcagcaagagagcactggcagaaaac 1221
DB 238 AAGGAGACATGTAAACAGAGTAAACATGTGTGAAGCAGCAAAAGAGGACACTGGCAGAAAAC 297
QY 1222 aaactgaacctctccaaagatgctgaaagagatggatgcttccaatctgattcaatgag 1281
DB 298 AACCTGAACCTTCCAAAGATGGCTGAAAAGATGGATGCTTCAATCTGGATTCAATGAG 357
QY 1282 gagacttgctggtgaaaaatcatcactggtctctttggagtttgaggtatataccttagagtag 1341
DB 358 GAGACTTGCTGGTGAATAATCATCACTGCTCTTTTGGAGTTTGAGGTATACCTAGAGTAC 417
QY 1342 ctccggaacagatttgagagtagtgaggaaacagccagagctgtgcagatgagtagcaaaa 1401
DB 418 CTCGAGAACAGATTTGAGAGTAGTGAGGAACAAAGCCAGAGCTGTGCAGATGATGACAAA 477
QY 1402 gtccgatccagttctcagaaaaagcagaagatcttagatgcaataaccacccctgac 1461
DB 478 GTCTGTATCCAGTCTCTGAGAAAAGGCAAGAAATCTAGATGCAATACCAACCCCTGAC 537
QY 1462 ccaaccacaaatgccagcctgctgacgaagctgcagggcagacaaacagtggtgctgcaggac 1521
DB 538 CCAACCACAAATGCCAGCCTGTGAGAAAGCTGCAGGCACAGAACCAAGTGGCTGCAGGAC 597
QY 1522 atgacaactcatctattctgcgagctttaaggagtttaaggagttcctgcagtcagccctgagggct 1581
DB 598 ATGACAACCTCATCTATTCTGGCGAGCTTTAAGGAGTTCTCTGCAGTCCAGCCTGAGGGCT 657
QY 1582 ctccggcaaatgtagcatgggcaccgtcga 1611
DB 658 CTTCCGCAAAATGTAGCATGGGCACCTCAGA 687

RESULT 14
E03737
LOCUS E03737 1102 bp RNA PAT 29-SEP-1997
DEFINITION CDNA encoding human B-cell differentiation factor.
ACCESSION E03737
VERSION E03737.1 GI:2171952
KEYWORDS JP 1992169599-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 1102)
Yasuda,H., Nagase,K., Kawai,M., Fukuhara,K. and Matsui,Y. .
VARIANT HUMAN BCF
TITLE
JOURNAL Patent: JP 1992169599-A 1 17-JUN-1992;
AJINOMOTO CO INC
COMMENT OS Homo sapiens (human)
PN JP 1992169599-A/1

PD 17-JUN-1992
PF 30-OCT-1990 JP 1990290704
PI YASUEDA HISASHI, NAGASE KAZUO, KAWAI MISAOKO, FUKUHARA KENICHI,
PI MATSUI YUTAKA
PC C07K13/00,C12N15/24,C12P21/02//A61K37/02,A61K37/02,A61K37/02,
PC (C12P21/02,
PC C12R1:19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
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FT CDS 36..674
FT /product='B-cell differentiation factor' FT
FT sig_peptide 36..119
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FT 3'UTR 675..1102.
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source
Location/Qualifiers
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/organism='Homo sapiens'
/db_xref='taxon:9606'
BASE COUNT 336 a 238 c 226 g 302 t
ORIGIN
Query Match 35.1%; Score 565.2; DB 5; Length 1102;
Best Local Similarity 99.5%; Pred. No. 7.8e-126;
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1042 cagtagtccccaggagaagattccaaagatgtagccgccccacacagacagcactcacc 1101
DB 120 CCAGTACCCCGAGGAGAAATTCCAAAGATGTAGCGCGCCACACAGACAGCCACTCACC 179
QY 1102 tcttcagaacgaattgacaaaataatcggtacatctctcagcggcatctcagccctgaga 1161
DB 180 TCTTCAGAACGAATTGACAAACAAATTCGGTACATCTCGACGGCATCTCAGCCCTGAGA 239
QY 1162 aaggagacatgtaaacagagtaacatgtgtgaagcagcaaaagagcactgggcagaaaac 1221
DB 240 AAGGAGACATGTAAACAGAGTAAACATGTGTGAAGCAGCAAAAGGACACTGGCAGAAAAC 299
QY 1222 aaactgaacctctccaaagatggctgaaaaagatggatgcttcccaatctgagtttaagt 1281
DB 300 AACCTGAACCTTCCAAAGATGGCTGAAAAGATGGATGCTTCCAATCTGGATTCAATGAG 359
QY 1282 gagacttgctggtgaaaaatcatcactggtcttttggagtttgaggtatataccttagagtag 1341
DB 360 GAGACTTGCTGTGTGAAATTCATCACTGGTCTTTTGGAGTTTGAGGTATACCTAGAGTAC 419
QY 1342 ctccagaacagatttgagagtagtgaggaacaagcagagcgtgtgcagatgagtagcaaaa 1401
DB 420 CTCAGACACAGATTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAA 479
QY 1402 gtccgtatccagttcctgcagaaaaaggcaagaatctagatgcaataaccacccctgac 1461
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QY 1462 ccaaccacaaatccagcctgctgacgaagctcagggcagacagacagcactggctgagagac 1521
DB 540 CCAACCACAAATGCCAGCCTGCTGACGAAGCTGCAGGCACAGAACCAAGTGGCTGCAGGAC 599
QY 1522 atgacaactcatctattctgcgagctttaaggagtttctcagtcagtcacccctgagggct 1581
DB 600 ATGACAACCTCATCTCATTTCTGCCAGCTTTAAGGAGTTCTCTGCAGTCCAGCCTGAGGGCT 659
QY 1582 ctccggcaaatgtagcatgggcaccgtcga 1611
DB 660 CTTCCGCAAAATGTAGCATGGGCACCTCAGA 689

RESULT 15
LOCUS HUMIL6C 1102 bp mRNA PRI 06-JAN-1995
DEFINITION Human interleukin 6 (B-cell stimulatory factor-2) mRNA, complete cds.
ACCESSION M29150.1 GI:186349
VERSION B-cell stimulatory factor-2; BSF-2; cytokine; interleukin 6;
KEYWORDS transmembrane glycoprotein.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1102)
AUTHORS Tonouchi, N., Miwa, K., Karasuyama, H. and Matsui, H.
TITLE Deletion of 3' untranslated region of human BSF-2 mRNA causes
stabilization of the mRNA and high-level expression in mouse NIH3T3 cells
JOURNAL Biochem. Biophys. Res. Commun. 163 (2), 1056-1062 (1989)
MEDLINE 89391958
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QPTSSRIDKQIRYILDGILSKRCKNSKNCESKEALNNLNLPKAEKDGCF
QSGNEETCLVKIITLLEFEVLYEIQNRFESSEQARAVQMSTKVLIOFLQKKKN
LDAITTPDTTNASLTKLQAQNWLDQMTTHILRSFKFEFLQSLRLRQM"
BASE COUNT 336 a 238 c 226 g 302 t
ORIGIN
Query Match 35.1%; Score 565.2; DB 10; Length 1102;
Best Local Similarity 99.5%; Pred. No. 7.8e-126;
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1042 ccagtagcccccaggagaagattccaagatgtagccgccccacacagacagccactcacc 1101
Db 120 CCAGTACCCCCCAGGAGAAGATTCCAAAGATGTAGCCGCCCCACACAGACAGCCACTCACC 179
QY 1102 tcttcagacgaattgacaacaattcgttacatcctcgacgcgcattcagccctgaga 1161
Db 180 TCTTCAGAACGAATTGACAAACAATTTCGGTACATCTCTGACGGGCATCTCAGCCCTGAGA 239
QY 1162 aaggagacatgaacaagagtaacatgtgtgaaagcagcaaaaggcagcctggcagaaaaac 1221
Db 240 AAGGAGACATGTAAACAGAGTAACATGTGTAAAGACAGCAAAAGAGGCACCTGGCAGAAAAAC 299
QY 1222 aacctgaacctccaaagatggctgaaaagatgagatgcttccaatctggattcaatgag 1281
Db 300 AACCTGAACCTTCCAAAGATGGCTGAAAAGATGGATGCTTCCAAATCTGGATTCAATGAG 359
QY 1282 gagacttgcctgtgaaaatactcactggctcttttggagtttgaggtatccttagagtac 1341
Db 360 GAGACTTGCTGTGGAATAATCATCAGTGGCTTTTGGAGTTTGAGGTATACCTAGAGTAC 419
QY 1342 ctccagacagatttgagtagtgaggaacaagccagagctgtgcagatgagtacaaaa 1401
Db 420 CTCAGAACAGATTGTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAAA 479
QY 1402 gtctgtatccagttctctgcgagaaaaaggcaagaatctagatgaataaccacctgtac 1461

Db 480 GTCTGTATCCAGTTCTCTGCAGAAAAAGCAAGAATCTAGATGCAATAACCCCTGAC 539
QY 1462 ccaaccacaaatgccagcctgtgacgaagctgcaggcacagaaacagtggtgctgcaggac 1521
Db 540 CCAACCAAAATGCCAGCCTGCTGACGAAGCTGCAGGACACAGAACCACTGGCTGCAGGAC 599
QY 1522 atgacaaatcattctcattctgcgaagctttaagagagttcctgcagtcagcctgagggct 1581
Db 600 ATGACAACCTCATCTCATTTCTGCGCAGCTTTAAGGAGTTCTCTGCAGTCCAGCTGAGGGCT 659
QY 1582 cttoaggcaaatgtagcatgggcacacctga 1611
Db 660 CTTCGGCAAAATGTAGCATGGGCACCTCAGA 689

Search completed: August 9, 2000, 07:07:22
Job time: 62356 sec

WIREH (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Aug 10 16:16:47 2000; MasPar time 40.07 Seconds
Tabular output not generated. 899.809 Million cell updates/sec

Title: >US-09-142-471-4
Description: (1-520) from US09142471.pep
Perfect Score: 3771
Sequence: 1 MLAVGCALLAALLAAPCAAL.....LILSPKFEQLQSSLRALRQM 520

Scoring table: PAM 150
Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl12
1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 50.078; Variance 91.622; scale 0.547

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	1320	35.0	440 11	Q00343	INTERLEUKIN 6 RECEPTOR	1.90e-260
2	1239	32.9	209 6	Q97540	INTERLEUKIN-6 (FRAGMEN	6.06e-242
3	814	21.6	209 6	Q28819	INTERLEUKIN 6 (FRAGMEN	7.29e-146
4	810	21.5	205 6	Q28747	INTERLEUKIN 6 (FRAGMEN	5.70e-145
5	804	21.3	208 6	Q9XT80	INTERLEUKIN 6 PRECURSO	1.25e-143
6	748	19.8	160 6	Q97535	INTERLEUKIN-6 (FRAGMEN	3.66e-131
7	725	19.2	207 6	Q28403	INTERLEUKIN 6 (FRAGMEN	4.64e-126
8	539	14.3	210 11	Q9WV08	IL-6 (FRAGMENT)	2.71e-85
9	415	11.0	372 11	Q88507	CILIARY NEUROTROPHIC F	7.68e-59
10	406	10.8	432 11	Q64385	INTERLEUKIN-11 RECEPTO	5.91e-57
11	401	10.6	432 11	P70225	INTERLEUKIN-11 RECEPTO	6.57e-56
12	397	10.5	66 6	Q18796	INTERLEUKIN 6 RECEPTOR	4.50e-55
13	337	10.5	422 4	Q16542	INTERLEUKIN-11 RECEPTO	4.50e-55
14	381	10.1	94 6	Q62775	INTERLEUKIN 6 (FRAGMEN	9.60e-52
15	329	8.7	101 11	O55041	INTERLEUKIN 6 (FRAGMEN	4.52e-41
16	252	6.7	204 14	O40918	ORF K2.	7.97e-26
17	252	6.7	204 14	Q98823	INTERLEUKIN-6 HOMOLOG	7.97e-26
18	202	5.4	422 4	O75462	CYTOKINE-LIKE FACTOR-1	1.83e-16
19	182	4.8	228 11	O35228	CYTOKINE RECEPTOR-LIKE	6.77e-13
20	180	4.8	581 6	O46561	PROLACTIN RECEPTOR LON	1.52e-12

21	179	4.7	296	6	O18880	PROLACTIN RECEPTOR SHO	2.27e-12
22	168	4.5	229	4	O75269	HUMAN CYTOKINE RECEPTO	1.78e-10
23	163	4.3	229	4	O14213	CYTOKINE RECEPTOR PREC	1.25e-09
24	161	4.3	346	13	O93404	PROLACTIN RECEPTOR (FR	2.70e-09
25	151	4.0	335	6	P79203	PROLACTIN RECEPTOR (FR	1.21e-07
26	142	3.8	206	4	Q16354	PROLACTIN RECEPTOR (FR	3.37e-06
27	144	3.8	316	11	O35545	INTRON 5-INSERTED FORM	1.62e-06
28	130	3.4	217	6	O46386	PROLACTIN RECEPTOR (FR	2.43e-04
29	128	3.4	266	5	P91608	LIM DOMAIN PROTEIN BX	4.85e-04
30	130	3.4	329	6	Q9XSQ5	INTERLEUKIN 12 P40 SUB	2.43e-04
31	130	3.4	625	6	Q9XS92	PROLACTIN RECEPTOR PRE	2.43e-04
32	129	3.4	895	11	O62960	LEPTIN RECEPTOR.	3.43e-04
33	124	3.3	194	6	O02708	GLYNULOCYTE COLONY-STI	1.90e-03
34	124	3.3	229	6	O28206	ERYTHROPOIETIN RECEPTO	1.90e-03
35	124	3.3	229	6	Q27950	ERYTHROPOIETIN RECEPTO	1.90e-03
36	126	3.3	874	11	P97378	INTERLEUKIN 12 RECEPTO	9.65e-04
37	123	3.3	1165	6	O02671	TRANSMEMBRANE LEPTIN R	2.67e-03
38	119	3.2	796	13	Q91287	FIBROBLAST GROWTH FACT	1.01e-02
39	122	3.2	862	4	O99665	IL-12 RECEPTOR BETA2.	3.74e-03
40	122	3.2	881	13	O57519	GPI30P1.	3.74e-03
41	120	3.2	1250	11	O88971	CDO.	7.29e-03
42	121	3.2	1571	4	O60469	DOWN SYNDROME CELL ADH	5.22e-03
43	121	3.2	1896	4	O60468	DOWN SYNDROME CELL ADH	5.22e-03
44	118	3.1	1240	4	O14631	CDO.	1.41e-02
45	118	3.1	5198	5	O76518	HEMICENTIN PRECURSOR.	1.41e-02

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	440 AA.
AC	Q00343			
DT	01-NOV-1996 (Tremblrel. 01, Created)			
DT	01-NOV-1996 (Tremblrel. 01, Last sequence update)			
DT	01-NOV-1999 (Tremblrel. 12, Last annotation update)			
DE	INTERLEUKIN 6 RECEPTOR, ALPHA PRECURSOR			
DE	(MUTANT INTERLEUKIN-6 RECEPTOR).			
OS	IL6RA.			
GN	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN-BALB/C.			
RX	MEDLINE: 90278354.			
RA	SUGITA T., TORSUKA T., SAITO M., YAMASAKI K., TAGA T., HIRANO T.,			
RA	KISHIMOTO T.;			
RT	*Functional murine interleukin 6 receptor with the intracisternal A			
RT	particle gene product at its cytoplasmic domain. Its possible role in			
RT	plasmacytomagenesis."			
RL	J. Exp. Med. 171:2001-2009(1990).			
CC	-I- MISCELLANEOUS: THIS PROTEIN IS A ABNORMAL INTERLEUKIN-6 RECEPTOR.			
CC	IN THE CDNA ENCODING THE ABNORMAL INTERLEUKIN-6 RECEPTOR THE			
CC	REGION CORRESPONDING TO ITS INTRACYTOPLASMIC DOMAIN WAS REPLACED			
CC	WITH A LONG TERMINAL REPEAT OF THE INTRACISTERNAL A PARTICLE (IAP)			
CC	GENE. A MEMBER OF THE ENDOGENOUS PRORETROVIRAL-LIKE ELEMENTS			
CC	PRESENT IN THE GENOME OF MUS MUSCULUS.			
DR	EMBL: X51976; CAA36238.1; -.			
DR	PIR: JLO144; JLO144.			
DR	HSSP: PI4787; IAN3.			
DR	MGI: 105304; IL6ra.			
DR	PFAM: PF00041; fn3; 1.			
DR	PFAM: PF00047; ig; 1.			
KW	Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.			
FT	SIGNAL 1 19			
FT	CHAIN 20 440			
FT	DOMAIN 1 385			
FT	DOMAIN 20 357			
FT	DOMAIN 43 36			
FT	DOMAIN 385 385			
FT	TRANSMEM 386 440			
FT	DOMAIN 386 440			
FT	DOMAIN 386 440			
FT	DISULFID 47 92			

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FT CARBOHYD 32 32 POTENTIAL.
FT CARBOHYD 55 55 POTENTIAL.
FT CARBOHYD 150 150 POTENTIAL.
SQ SEQUENCE 440 AA; 47901 MW; EBS7B93 CRC32;

Query Match 35.0%; Score 1320; DB 11; Length 440;
Best Local Similarity 55.1%; Pred. No. 1.90e-260;
Matches 179; Conservative 58; Mismatches 82; Indels 6; Gaps 3;

Db 1 MLTVCCTLLVALLAVALVGLSCRALEVANGIVTSLPGATVVLICPGKEAAGNTIHW 60
Qy 1 MLVACALLAALLAAGAAAPRCPAQEVARGVLTSLPGSDVLTLCGVEPEDNATVHW 60
Db 61 VY----SGSQNREWTTCNTLVLDVQLSDGTYLCSLNDHLVGTPLVLLVDPPEEPKLS 116
Qy 1 VLRPAAGSHPSRWAGMGRLLRSVQLHSDNSYSCYRAGPAGTVHLLVDPPEEPOLS 120
Db 117 CFRKNPLVNAICEWRSPSTPPTKAVLFAKKINTNGSKDFQVPCQYSQQLKSFSCOVE 176
Qy 121 CFRKSPLSNVVCWGPSTPSTLITKAVLLVRKFQNSPAE-DFQEPQCYQSQSKFSCOLA 179
Db 177 ILEGDKVHYIYSLCVANSVSGSKSHNEAFHSIKWQVDPDPANLVYSAIPGRWLKYSWQ 236
Qy 180 VPEGSSYIIVSMCVASSVSGSKFTQFGCGILQPPPANITVAVARNPRLSVTWQ 239
Db 237 HPETWDPYSYLLQFLRYPVMSKEFTVLLLPVAYQCYQVIHDLRGVYVQVRGKEELD 296
Qy 240 DPHSNWSFYRLRELRYRAERSKFTTVMYKDLQHHCVIHDAMSLGRHVQLRAQBEFG 299
Db 297 LGQWSEWSPVETGPTWIAEPRTTA 321
Qy 300 QGEWSEWSPVETGPTWIAEPRTTA 323

RESULT 2 PRELIMINARY; PRT; 209 AA.
ID O97540;
AC O97540;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus nancyanae (Owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
RN SEQUENCE FROM N.A.
RA EGHEVERRY S.J., HERNANDEZ E., MORENO A., PATAROTO M.E., MURILLO L.A.;
RT "Identification, cloning and sequencing of different interleukin genes
in 4 Aotus species.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014510; AAD01536.1; -.
DR HSP; P05231; IALU.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1 1
FT SEQUENCE 209 AA; 23406 MW; 99D77053 CRC32;

Query Match 32.9%; Score 1239; DB 6; Length 209;
Best Local Similarity 97.2%; Pred. No. 6.06e-242;
Matches 176; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 29 PVPPGDSKEVAAPNRPOLSTSTEIDKIRYILDIGISALRKETCNKSNMCESSKEALAE 88
Qy 337 PVPPGDSKDVAAHPHQPLSSERIDKQIRYILDIGISALRKETCNKSNMCESSKEALAE 396
Db 89 NLNPKMAEKDGCQFSGFNEETCLVKITGLLEFEVYLEYLNRFESSEEQARAVQMSTK 148
Qy 397 NLNPKMAEKDGCQFSGFNEETCLVKITGLLEFEVYLEYLNRFESSEEQARAVQMSTK 456
Db 149 VLIOFLOKKAKNLDAITTPPTTNASLLTKLQAOQNLQDMTTHLILRSKEFLQSSIRA 208
Qy 457 VLIOFLOKKAKNLDAITTPPTTNASLLTKLQAOQNLQDMTTHLILRSKEFLQSSIRA 516

Query Match 21.6%; Score 814; DB 6; Length 209;
Best Local Similarity 59.2%; Pred. No. 7.29e-146;
Matches 109; Conservative 35; Mismatches 40; Indels 0; Gaps 0;

Db 26 PGVPVGSQADATSNRPPLSPDRKMEFIKYLKISALRKEMCDKYNKCEDSKAEALAE 85
Qy 337 PVPPGDSKDVAAHPHQPLSSERIDKQIRYILDIGISALRKETCNKSNMCESSKEALAE 396
Db 86 NLRLPKLAEKDGCQFSGFNEETCLVKITGLLEFEVYLEYLNRFESSEEQARAVQMSTK 145
Qy 397 NLNPKMAEKDGCQFSGFNEETCLVKITGLLEFEVYLEYLNRFESSEEQARAVQMSTK 456
Db 146 LLVOMLAKKVKQSDQEVTPPTTTSQAILKADQKWLKHTTTHLILRSKEFLQSSIRA 205
Qy 457 VLIOFLOKKAKNLDAITTPPTTNASLLTKLQAOQNLQDMTTHLILRSKEFLQSSIRA 516
Db 206 VRIM 209
Qy 517 LRQM 520

RESULT 4 PRELIMINARY; PRT; 205 AA.
ID Q28747;
AC Q28747;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Orcinus orca (killer whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae; Orcinus.
RN SEQUENCE FROM N.A.
RA KING D.P., SCHRENZEL M.D., MCKNIGHT M.L., REIDARSON T.H., HANNI K.D.,
STOTT J.L., FERRICK D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
Southern sea otter (Enhydra lutris nereis).";

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RL Immunogenetics 43:190-195(1996).
DR EMBL; L46803; AAB01429.1; -.
DR HSP; P05231; 1ALU.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR PFAM; PF00489; IL-6; 1.
FT NON_TER 1
SQ SEQUENCE 205 AA; 23266 MW; C853C8DF CRC32;

Query Match
Best Local Similarity 21.5%; Score 810; DB 6; Length 205;
Matches 111; Conservative 36; Mismatches 35; Indels 1; Gaps 1;

Db 21 PGPGLGDFKDDTSRLYLTSPDKTEALIKYILGKISAMRKEMCEKYDKCNSKEALAEN 80
QY 337 PVPVGGDSKDVAAAPHRQPLTSSERIDKQIRYILDGTSALRKETCNKSNMCCSKEALAEN 396
Db 81 NLNLPKMAEKDCGFCGSGFNQETCLMRITTTGLLEYQIYLDYQNEVYEGDKGAEAVQISK 140
QY 397 NLNLPKMAEKDCGFCGSGFNQETCLMRITTTGLLEYQIYLDYQNEVYEGDKGAEAVQISK 140
Db 141 ALAQILROKVKNPDEVTTPDPTTNASLMNLOSQNDWMKNTKIILRLSLENFLQFSLR 200
QY 457 VLIQFLQKAKKALDAITTPDPTTNASLLTKLQAQNO-WLQDWTTHLLRSFKREFLOSSLR 515
Db 201 AIR 203
QY 516 ALR 518

RESULT 5
ID Q9XT80 PRELIMINARY; PRT; 208 AA.
AC Q9XT80;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE INTERLEUKIN 6 PRECURSOR.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Monodontidae;
OC Delphinapterus.
RN [1]
RP SEQUENCE FROM N.A.
RA ST-LAURENT G., DE GUISE S., FOURNIER M., ARCHAMBAULT D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) interleukin 6."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076643; AAD42929.1; -.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 208 AA; 23456 MW; OFA70646 CRC32;

Query Match
Best Local Similarity 21.3%; Score 804; DB 6; Length 208;
Matches 110; Conservative 36; Mismatches 36; Indels 1; Gaps 1;

Db 24 PGPGLGDFKDDTSRLYLTSPDKTEALIKYILGKISAMRKEMCEKYDKCNSKEALAEN 83
QY 337 PVPVGGDSKDVAAAPHRQPLTSSERIDKQIRYILDGTSALRKETCNKSNMCCSKEALAEN 396
Db 84 NLNLPKMAEKDCGFCGSGFNQETCLMRITTTGLLEYQIYLDYQNEVYEGDKGAEAVQISK 143
QY 397 NLNLPKMAEKDCGFCGSGFNQETCLMRITTTGLLEYQIYLDYQNEVYEGDKGAEAVQISK 143
Db 144 ALAQILROKVKNPDEVTTPDPTTNASLMNLOSQNDWMKNTKIILRLSLENFLQFSLR 203
QY 457 VLIQFLQKAKKALDAITTPDPTTNASLLTKLQAQNO-WLQDWTTHLLRSFKREFLOSSLR 515
Db 204 AVR 206
QY 516 ALR 518

RESULT 6
ID Q97535 PRELIMINARY; PRT; 160 AA.
AC Q97535;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus vociferans.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
RN [1]
RP SEQUENCE FROM N.A.
RA ECHEVERRY S.J., HERNANDEZ E., MORENO A., PATARROYO M.E., MURILLO L.A.;
RT "Identification, cloning and sequencing of different interleukin genes
RT in 4 Aotus species."
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014505; AAD01531.1; -.
DR HSP; P05231; 2IL6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1
SQ SEQUENCE 160 AA; 17855 MW; EF6090C3 CRC32;

Query Match
Best Local Similarity 19.8%; Score 748; DB 6; Length 160;
Matches 105; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Db 29 PVPVGGDSKDVAAAPHRQPLTSSERIDKQIRYILDGTSALRKETCNKSNMCCSKEALAEN 88
QY 337 PVPVGGDSKDVAAAPHRQPLTSSERIDKQIRYILDGTSALRKETCNKSNMCCSKEALAEN 396
Db 89 NLNLPKMAEKDCGFCGSGFNQETCLMRITTTGLLEYQIYLDYQNEVYEGDKGAEAVQISK 148
QY 397 NLNLPKMAEKDCGFCGSGFNQETCLMRITTTGLLEYQIYLDYQNEVYEGDKGAEAVQISK 148
Db 141 ALAQILROKVKNPDEVTTPDPTTNASLMNLOSQNDWMKNTKIILRLSLENFLQFSLR 200
QY 457 VLIQFLQKAKKALDAITTPDPTTNASLLTKLQAQNO-WLQDWTTHLLRSFKREFLOSSLR 515
Db 201 AIR 203
QY 516 ALR 518

RESULT 7
ID Q28403 PRELIMINARY; PRT; 207 AA.
AC Q28403;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Euhadra lutris (Sea otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Mustelidae; Enhydra.
RN [1]
RP SEQUENCE FROM N.A.
RA KING D.P., SCHRENZEL M.D., MCKNIGHT M.L., REIDARSON T.H., HANNI K.D.,
RA STOTT J.L., FERRICK D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:190-195(1996).
DR EMBL; L46804; AAB01428.1; -.
DR HSP; P05231; 2IL6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR PFAM; PF00489; IL-6; 1.
FT NON_TER 1
SQ SEQUENCE 207 AA; 23527 MW; OF2CACG2 CRC32;

Query Match
Best Local Similarity 19.2%; Score 725; DB 6; Length 207;
Matches 100; Conservative 42; Mismatches 40; Indels 2; Gaps 2;

Db 26 PGPGLGDSKDDTSNRPLTSSADKMEFDIKFGLKISALRNEMCDKYNKCEDSKVEALAEN 85
QY 337 PVPVGGDSKDVAAAPHRQPLTSSERIDKQIRYILDGTSALRKETCNKSNMCCSKEALAEN 396
Db 86 NLNLPKMAEKDCGFCGSGFNQETCLMRITTTGLQEQFQHLKYLESNYEGKNKNAHSVISTK 145
QY 397 NLNLPKMAEKDCGFCGSGFNQETCLMRITTTGLQEQFQHLKYLESNYEGKNKNAHSVISTK 145
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Db 146 HLLQTLRPM-NOIE-VTPDPPTDASLQALFKSQDKWLKHTTIHLIRLLEDLFQFSURA 203
QY 457 VLIQFLOKKAALDAITTPDPTTNASLLTKLQAQONQWLQDMTTHLILRSFKFLQSSURA 516
Db 204 IRIM 207
QY 517 LRQM 520

RESULT 8
ID Q9WVQ8 PRELIMINARY; PRT; 210 AA.
AC Q9WVQ8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE IL-6 (FRAGMENT).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=APA; TISSUE=KIDNEY;
RA NISHIDA E.;
RT "APA hamsters IL-6 partial cDNA.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB028635; BAA78766.1; -.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1
QY SEQUENCE 210 AA; 24060 MW; 0307F113 CRC32;

Query Match 14.3%; Score 539; DB 11; Length 210;
Best Local Similarity 38.8%; Pred. No. 2.71e-85;
Matches 71; Conservative 51; Mismatches 59; Indels 2; Gaps 2;

Db 28 VRRGDETD-TPNRPVYTSQVGGVTVVLYRELYELRKELCNPNPCMDNDVLLNN 86
QY 338 VPPGDSKDVAAHPHQPTSSERTDKQIRYILDGISAURKCTCNKSNCCSKKALAENN 397
Db 87 LELPVIQINDCLOTGVNWEICLKITSGLDYQIYLEFVTVNNVDNKKDKARVIQSTIK 146
QY 398 LNLPMKAEKDCFGSGFNEETCLVKITIGLLEFVLEYLQNR-ESSEEQARAVQSTK 456
Db 147 TLSQIFKQEVKPKIYTPSPSTSKAILMEKLESQKWPRTKILILKALEEFLEVTVMS 206
QY 457 VLIQFLOKKAALDAITTPDPTTNASLLTKLQAQONQWLQDMTTHLILRSFKFLQSSURA 516
Db 207 TRQ 209
QY 517 LRQ 519

RESULT 9
ID Q88507 PRELIMINARY; PRT; 372 AA.
AC Q88507;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR.
GN CNTRF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN, SKELETAL MUSCLE;
RA MAEDA M., YAGUCHI N., HANYUU C., NAKATA Y., ONODA N., TULIN E.E.,
RA KOJIMA T., HASEGAWA M., KIKUCHI Y., NOMURA H.;
RT "Mouse homolog of human ciliary neurotrophic factor receptor.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF068615; AAC25711.1; -.
DR PFAM; PF00041; fn3; 1.
DR PFAM; PF00047; ig; 1.
RT Signal.

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FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 336 CILIARY NEUROTROPHIC FACTOR RECEPTOR
FT ALPHA.
SQ SEQUENCE 372 AA; 40831 MW; 9A40FE12 CRC32;

Query Match 11.0%; Score 415; DB 11; Length 372;
Best Local Similarity 30.8%; Pred. No. 7.68e-59;
Matches 105; Conservative 81; Mismatches 131; Indels 24; Gaps 21;

Db 11 AVLAATAAAVYTKHQSPQEAHVQYERL-GADVTLPC-GTASWD-AAVTW--RVNGTDLA 65
QY 11 ALLAAPGAALAPRRCPAQEVARGLTSLPGDSVTLTCTPGVEPEDNATVHWLVRKPAAGSH 70
Db 66 PDLLG-SQ-LILRSLEIGHSGSLVACPHRDSWHLRHQVLLHVLGPPRPVPLSC-RSNYTP 122
QY 71 PSRWAGMGRULLRSVLQHDGNSYCY-RAGRAGTGVHLL-VDVPPPEQLSCFRKSPLS 128
Db 123 KGFYCSW-HLPTPTYPNT-FNVTVLHGS---KIMV-CE-KDPALKNRCHRYMHLEFSTI 175
QY 129 NVV-CWGPSTPSLTTKAVLLVRKFQNSPAEDFQEPQYQSQKFSQCLAVPEGDSF 187
Db 176 KYKVISISVSNALGN-TTATTFDEFTIVKPDPPENVARPVSPNRRLEVTVWQTPSTWPD 234
QY 188 -YIVSMCVASSVSGSKFSKTQTFQCGILQDPPANITVTAVARNRWLSVTWQDPHSW-N 245
Db 235 PESFPLKFLRYRLIILDOWHVELSDGTAH-TITDAVAGKEYITIOVAAKDN-EIGTWS 292
QY 246 SSFYELRFLRYRAERSKFTTVMVKDLOHCVIHDWSGLRHVVQLRAEEFGQGEWSE 305
Db 293 WSAHAATPMTPEPRHLTTAQAPETTTSTSSLAPPTTK 333
QY 306 WSPEAMGTPWTE-SRSPARGGGGGSGGSGVEPVPPGDSK 345

RESULT 10
ID Q64385 PRELIMINARY; PRT; 432 AA.
AC Q64385;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NR1) (ETL2)
DE (IL-11RALPHA) (IL11RAL).
GN IL11RAI OR IL11RA OR ETL2 OR ETL2/IL11 REC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=LIVER;
RX MEDLINE; 95045367.
RA HILTON D.J., HILTON A.A., RAICEVIC A., RAKAR S., HARRISON-SMITH M.,
RA GOUGH N.M., BEGLEY C.G., METCALF D., NICOLA N.A., WILLSON T.A.;
RT "Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130
RT for high affinity binding and signal transduction.";
RL EMBO J. 13:4765-4775(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C, AND C57BL/6; TISSUE=EMBRYO;
RA NEUHAUS H., BETTENHAUSEN B., BILINSKI P., SIMON-CHAZOTTES D.,
RA GUENET J.-L., GOSSLER A.;
RL Dev. Biol. 166:521-542(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C, AND C57BL/6;
RA GOSSLER A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97129000.
RA BILINSKI P., HALL M.A., NEUHAUS H., GISSEL C., HEATH J.K., GOSSLER A.;
RT "Two differentially expressed interleukin-11 receptor genes in the
RT mouse genome.";
RL Biochem. J. 320:359-363(1996).

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CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11. BINDS TO IL-11
 CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 DR EMBL: X74953; CAA52908.1; -
 DR EMBL: U14412; AA53248.1; -
 DR EMBL: X94162; CAA63873.1; -
 DR EMBL: X94163; CAA63873.1; JOINED.
 DR HSSP: P16471; 1BP3.
 DR MGD; MGI:107426; I111ra1.
 DR PFAM; PF00041; fn3; 2.
 DR PFAM; PF00047; ig; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 432
 FT DOMAIN 24 367
 FT TRANSMEM 368 393
 FT DOMAIN 394 432
 FT DOMAIN 41 102
 FT CARBOHYD 127 127
 FT CARBOHYD 194 194
 FT CONFLICT 384 384
 FT SEQUENCE 432 AA; 46655 MW; F65B3060 CRC32;
 Query Match 10.88; Score 406; DB 11; Length 432;
 Best Local Similarity 30.3%; Pred. No. 5.91e-57;
 Matches 110; Conservative 79; Mismatches 155; Indels 19; Gaps 18;
 Db 1 MSSSCSGLTRVLVAVATALVSSSPCPQAWGPPGVQGPGRVPLCCPGV-SAG-TPVS 58
 QY 2 LAVGCCALLAALAAAGALAPRCP-AQE-VARGVLTSLPGDSVTLTCGVEPEDNATVH 59
 Db 59 W-FRDGDSRLLOQPSDGLGHLRLVLAQVSDPGTYVCOITLDGVSGGMVTLKLGFPARPE 117
 QY 60 WVLKRPAGSHPSRWAGMGRLLRLSLVQLHDSGNSCYR-AGRPACTVHLLVDVPEEPQ 118
 Db 118 VSC-QAVDYENFSCWSPQVSGSLPRLYLTYSRK-KTLPGAESQRESPTSGMPCPQDPL 175
 QY 119 LSCFRKSPLSNVVCEWGPSTSLTTKAVLLVRKFQNSPAEDFQ-EPCQYSQ-E-SQK-F 174
 Db 176 EASRCVVHGAEFSEYRINVTENPLGASTCLLDVRLQ-SILRPPDPQGLRVESVPGYPR 234
 QY 175 -SCQLAVPEGD-SSFYIVSMCVASSVSGSKFTQTFQGGILQDPDPANITVAVARNR 232
 Db 235 RLHASTYTPASRRORPHFLKRLQYRPAQHPAWSTVEPIGLEE--VITDAVAGLPHAYR 292
 QY 233 WLSVTWQDPHSWNS-SFYRLRFELRYRAERSKFTFTTMVKDLQHHCVIHDWSGLRHVVQ 291
 Db 293 VSADEFLDAGTWSANSPAWGTFPSTGPL-QDEIPDWSQGHQQLAVVAQEDSPAPRPS 351
 QY 292 LRAEEFGQGEWSPEAMGTPWTESRPPARGGGGGGGGVPEVPVPEGDSKDVAAAPH 351
 Db 352 LQP 354
 QY 352 ROP 354

RESULT 11

ID P70225 PRELIMINARY; PRT; 432 AA.
 AC P70225; 009074;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 02, Last annotation update)
 DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 2 PRECURSOR (IL11RA2)
 DE (IL-11BETA) (INTERLEUKIN-11 RECEPTOR BETA CHAIN).
 GN IL11RA2 OR IL-11BETA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-CD1; TISSUE-TESTIS;
 RX MEDLINE; 97129000.
 RA BLINKSKI P., HALL M.A., NEUHAUS H., GISSEL C., HEATH J.K., GOSSLER A.;
 RT "Two differentially expressed interleukin-11 receptor genes in the
 RL mouse genome.";
 RL Biochem. J. 320:359-363(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD-1; TISSUE-TESTIS;
 RX MEDLINE; 96278810.
 RA ROBB L., HILTON D.J., WILLSON T.A., BEGLEY C.G.;
 RT "Structural analysis of the gene encoding the murine interleukin-11
 RT receptor alpha-chain and a related locus.";
 RL J. Biol. Chem. 271:13754-13761(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD-1; TISSUE-TESTIS;
 RX MEDLINE; 97230451.
 RA ROBB L., HILTON D.J., BROOK-CARTER P.T., BEGLEY C.G.;
 RT "Identification of a second murine interleukin-11 receptor alpha-chain
 RT gene (IL11ra2) with a restricted pattern of expression.";
 RL Genomics 40:387-394(1997).
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 DR EMBL: X94157; CAA63872.1; -
 DR EMBL: X94158; CAA63872.1; JOINED.
 DR EMBL: X94159; CAA63872.1; JOINED.
 DR EMBL: X94160; CAA63872.1; JOINED.
 DR EMBL: X94161; CAA63872.1; JOINED.
 DR EMBL: X98519; CAA67144.1; -
 DR EMBL: U69491; AAC53114.1; -
 DR HSSP: P16471; 1BP3.
 DR MGD; MGI:109123; I111ra2.
 DR PFAM; PF00041; fn3; 2.
 DR PFAM; PF00047; ig; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 432
 FT DOMAIN 24 367
 FT TRANSMEM 368 393
 FT DOMAIN 394 432
 FT DOMAIN 41 102
 FT CARBOHYD 127 127
 FT CARBOHYD 194 194
 FT CONFLICT 200 200
 FT CONFLICT 384 384
 FT SEQUENCE 432 AA; 46721 MW; C4FD7DEC CRC32;
 Query Match 10.68; Score 401; DB 11; Length 432;
 Best Local Similarity 30.3%; Pred. No. 6.57e-56;
 Matches 110; Conservative 79; Mismatches 155; Indels 19; Gaps 18;
 Db 1 MSSSCSGLTRVLVAVATALVSSSPCPQAWGPPGVQGPGRVPLCCPGV-SAG-TPVS 58
 QY 2 LAVGCCALLAALAAAGALAPRCP-AQE-VARGVLTSLPGDSVTLTCGVEPEDNATVH 59
 Db 59 W-FRDGDSRLLOQPSDGLGHLRLVLAQVSDPGTYVCOITLDGVSGGMVTLKLGFPARPE 117
 QY 60 WVLKRPAGSHPSRWAGMGRLLRLSLVQLHDSGNSCYR-AGRPACTVHLLVDVPEEPQ 118
 Db 118 VSC-QAVDYENFSCWSPQVSGSLPRLYLTYSRK-KTLPGAESQRESPTSGMPCPQDPL 175
 QY 119 LSCFRKSPLSNVVCEWGPSTSLTTKAVLLVRKFQNSPAEDFQ-EPCQYSQ-E-SQK-F 174
 Db 176 EASRCVVHGAEFSEYRINVTENPLGASTCLLDVRLQ-SILRPPDPQGLRVESVPGYPR 234
 QY 175 -SCQLAVPEGD-SSFYIVSMCVASSVSGSKFTQTFQGGILQDPDPANITVAVARNR 232

Db 61 LOSQEWLHRTHTLRLKLEDFLOFSLRVRIM 94
 QY 487 LQAQNOWLQDMTHILRSFKFLOSSLRALROM 520

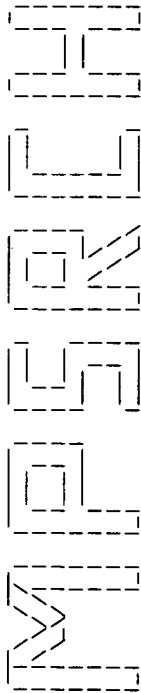
RESULT 15
 ID O55041 PRELIMINARY; PRT; 101 AA.
 AC O55041;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE INTERLEUKIN 6 (FRAGMENT).
 GN IL-6.
 OS Cricetulus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HEINE H., DELODE R.D., MONKS B., GOLENBOCK D.T.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF044667; AAC02100.1; -.
 DR HSSP; P05231; 2IL6.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR PFW; PF00489; IL-6; 1.
 FT NON_TER 1
 FT NON_TER 101
 SQ SEQUENCE 101 AA; 11749 MW; DIDA362A CRC32;

Query Match 8.7%; Score 329; DB 11; Length 101;
 Best local Similarity 41.2%; Pred. No. 4.52e-41;
 Matches 40; Conservative 28; Mismatches 28; Indels 1; Gaps 1;

Db 5 NDGCYOTGYNWEICLLKITSGLDYIYLEFVTNNVQDNKKDKARVIOSTTKTLQIFKQ 64
 QY 406 KGCCTQSGFNETCLVKITGLLEFEVYLEYIQNRF-ESSEQARAVQMSTKVLIOFLQK 464
 Db 65 EVKDPDKIVMPSPSKAILIEKLESQKQMPRTKTIEL 101
 QY 465 KAKNLDAITTPDPTTNASLLTKLQAQNOWLQDMTHL 501

Search completed: Thu Aug 10 16:19:18 2000
 Job time : 151 secs.

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(TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Aug 10 16:15:35 2000; MasPar time 17.31 Seconds
Tabular output not generated. 930.844 Million cell updates/sec

Title: >US-09-142-471-4
Description: (1-520) from US09142471.ppe
Perfect Score: 3771
Sequence: 1 MIAVGCALLAALLAAPGAAL.....LILRSFKFQLQSSLRALRQM 520

Scoring table: PAM 150
Gap 11

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot38
1:swissprot

Statistics: Mean 50.665; Variance 86.177; scale 0.588

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2398	63.6	468	1 IL6A_HUMAN	INTERLEUKIN-6 RECEPTOR	0.00e+00
2	1361	36.1	462	1 IL6A_RAT	INTERLEUKIN-6 RECEPTOR	2.44e-230
3	1320	35.0	460	1 IL6A_MOUSE	INTERLEUKIN-6 RECEPTOR	2.98e-280
4	1287	34.1	212	1 IL6_MACAU	INTERLEUKIN-6 PRECURSOR	3.84e-272
5	1257	33.3	212	1 IL6_MACAU	INTERLEUKIN-6 PRECURSOR	8.91e-265
6	1251	33.2	212	1 IL6_MACAU	INTERLEUKIN-6 PRECURSOR	1.34e-263
7	1244	33.0	212	1 IL6_MACAU	INTERLEUKIN-6 PRECURSOR	1.34e-261
8	814	21.6	209	1 IL6_MOUSE	INTERLEUKIN-6 PRECURSOR	4.33e-157
9	810	21.5	205	1 IL6_MOUSE	INTERLEUKIN-6 PRECURSOR	3.95e-156
10	806	21.4	208	1 IL6_MOUSE	INTERLEUKIN-6 PRECURSOR	3.60e-155
11	801	21.2	212	1 IL6_MOUSE	INTERLEUKIN-6 PRECURSOR	5.69e-154
12	786	20.8	207	1 IL6_MOUSE	INTERLEUKIN-6 PRECURSOR	2.23e-150
13	786	20.8	208	1 IL6_MOUSE	INTERLEUKIN-6 PRECURSOR	2.23e-150
14	693	18.4	208	1 IL6_MOUSE	INTERLEUKIN-6 PRECURSOR	3.34e-128
15	683	18.1	208	1 IL6_MOUSE	INTERLEUKIN-6 PRECURSOR	7.87e-126
16	680	18.0	208	1 IL6_MOUSE	INTERLEUKIN-6 PRECURSOR	4.05e-125
17	654	17.3	207	1 IL6_MOUSE	INTERLEUKIN-6 PRECURSOR	5.75e-119
18	560	14.9	211	1 IL6_MOUSE	INTERLEUKIN-6 PRECURSOR	6.70e-97
19	558	14.8	211	1 IL6_MOUSE	INTERLEUKIN-6 PRECURSOR	1.96e-96
20	491	13.0	125	1 IL6_MOUSE	INTERLEUKIN-6 (IL-6) (6.39e-81
21	409	10.8	372	1 CNTR_RAT	CILIARY NEUROTROPHIC F	2.94e-62
22	408	10.8	372	1 CNTR_HUMAN	CILIARY NEUROTROPHIC F	4.93e-62
23	373	9.9	362	1 CNTR_CHICK	CILIARY NEUROTROPHIC F	3.26e-54

24	212	5.6	831	1 PRLR_CHICK	PROLACTIN RECEPTOR PRE	4.07e-20
25	205	5.4	831	1 PRLR_MELGA	PROLACTIN RECEPTOR PRE	9.58e-19
26	179	4.7	201	1 MGE_CHICK	MYELOMONOCYTIC GROWTH	8.79e-14
27	179	4.7	581	1 PRLR_BOVIN	PROLACTIN RECEPTOR PRE	8.79e-14
28	172	4.6	830	1 PRLR_COLLI	PROLACTIN RECEPTOR PRE	1.73e-12
29	165	4.4	630	1 PRLR_ORENI	PROLACTIN RECEPTOR PRE	3.27e-11
30	155	4.1	917	1 IL6_MOUSE	INTERLEUKIN-6 RECEPTOR	1.98e-09
31	152	4.0	616	1 PRLR_RABIT	PROLACTIN RECEPTOR PRE	6.65e-09
32	144	3.8	622	1 PRLR_HUMAN	PROLACTIN RECEPTOR PRE	1.59e-07
33	140	3.7	610	1 PRLR_RAT	PROLACTIN RECEPTOR PRE	7.51e-07
34	141	3.7	918	1 IL6_MOUSE	INTERLEUKIN-6 RECEPTOR	5.10e-07
35	139	3.7	918	1 IL6_MOUSE	INTERLEUKIN-6 RECEPTOR	1.10e-06
36	137	3.6	581	1 PRLR_CEREL	PROLACTIN RECEPTOR PRE	2.37e-06
37	137	3.6	608	1 PRLR_MOUSE	PROLACTIN RECEPTOR PRE	2.37e-06
38	128	3.4	327	1 IL2B_MOUSE	INTERLEUKIN-12 BETA CH	6.92e-05
39	127	3.4	328	1 IL2B_HUMAN	INTERLEUKIN-12 BETA CH	9.99e-05
40	130	3.4	329	1 IL2B_MOUSE	INTERLEUKIN-12 BETA CH	3.31e-05
41	129	3.4	1162	1 LEPR_RAT	LEPTIN RECEPTOR PRECUR	4.79e-04
42	124	3.3	194	1 CSF3_FELCA	GRANULOCYTE COLONY-STI	2.97e-04
43	126	3.3	329	1 IL2B_FELCA	INTERLEUKIN-12 BETA CH	1.44e-04
44	126	3.3	329	1 IL2B_CANFA	INTERLEUKIN-12 BETA CH	1.44e-04
45	126	3.3	4393	1 PGBM_HUMAN	BASEMENT MEMBRANE-SPEC	1.44e-04

ALIGNMENTS

RESULT 1	IL6A_HUMAN	STANDARD;	PRT;	468 AA.
AC	P08887;			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	01-NOV-1988 (Rel. 09, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (CD126 ANTIGEN).			
DE	IL6R.			
GN	IL6R.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 88305347.			
RA	Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B., Taniguchi T., Hirano T., Kishimoto T.;			
RA	"Cloning and expression of the human interleukin-6 (BSP-2/IFN beta 2) receptor".			
RT	Science 241:825-828(1988).			
RL	[2]			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B., Taniguchi T., Hirano T., Kishimoto T.;			
RA	"Molecular structure of interleukin 6 receptor".			
RL	Proc. Jpn. Acad., B, Phys. Biol. Sci. 64:209-211(1988).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 91336983.			
RA	Schoellink H., Stoyan T., Lenz D., Schmitz H., Hirano T., Kishimoto T., Heinrich P.C., Rose-John S.;			
RA	"Structural and functional studies on the human hepatic interleukin-6 receptor. Molecular cloning and overexpression in HepG2 cells."			
RT	Biochem. J. 277:659-664(1991).			
RL	CC			
CC	- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL.			
CC	- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.			
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.			
CC	- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC	- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.			
CC	- DATABASE: NAME=PROW; NOTE=CD guide CD126 entry;			
CC	WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd126.htm"			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its			

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EMBL; X12830; CAA31312.1; -
EMBL; X58298; CAA41231.1; -
PIR; A41242; A41242.
PIR; J00080; J00080.
PIR; S14621; S14621.
PIR; S17468; S17468.
MIM; 147880; -
PFAM; PF00041; fn3; 1.
PFAM; PF00047; ig; 1.
PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.

Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat; Signal.

INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
POTENTIAL.
BY SIMILARITY.
DISULFID 121 132
DISULFID 165 176
CARBOHYD 55 55
CARBOHYD 93 93
CARBOHYD 221 221
CARBOHYD 245 245
CARBOHYD 350 350
POTENTIAL.
POTENTIAL.
SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1B8B CRC64;

Query Match 63.6%; Score 2398; DB 1; Length 468;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLAVGCALLAALLAAGAALAPRCPAQAEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Oy 1 MLAVGCALLAALLAAGAALAPRCPAQAEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNSCYRAGRAGTAVHLLVDPPEEPOLS 120
Oy 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNSCYRAGRAGTAVHLLVDPPEEPOLS 120
Db 121 CFRKSPNSVVCVCGPRSTPILTKAVLLVRKFQNSPAEDFQPCQYSOESQKSCQLAV 180
Oy 121 CFRKSPNSVVCVCGPRSTPILTKAVLLVRKFQNSPAEDFQPCQYSOESQKSCQLAV 180
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGIILQDPPANITVAVARNRWLSVTWQD 240
Oy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGIILQDPPANITVAVARNRWLSVTWQD 240
Db 241 PHSNNSFYRLRFELRYAERSKFTTWMVKDLQHCVHIDAWGLRHVQLRAQEFGQ 300
Oy 241 PHSNNSFYRLRFELRYAERSKFTTWMVKDLQHCVHIDAWGLRHVQLRAQEFGQ 300
Db 301 GEWSNPSPAMGTPTWTSRSPPA 323
Oy 301 GEWSNPSPAMGTPTWTSRSPPA 323

RESULT 2
ID IL6A.RAT STANDARD; PRT; 462 AA.
AC P22273;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA).
GN IL6R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
[1]
SEQUENCE FROM N.A.
STRAIN-FISCHER 344; TISSUE=LIVER;
EX MEDLINE; 91060602.
RA Baumann M., Baumann H., Fey G.H.;
RT "Molecular cloning, characterization and functional expression of the
RL rat liver interleukin 6 receptor";
J. Biol. Chem. 265:19853-19862(1990).
[2]
IDENTIFICATION OF PROBABLE FRAMESHIFT IN 227-261.
RP Gibson T.;
RA Unpublished observations (FEB-1995).

-!- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL.
-!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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EMBL; M58587; AAA41431.1; -
PIR; A37986; A37986.
HSP; P16471; 1BP3.
PFAM; PF00041; fn3; 1.
PFAM; PF00047; ig; 1.
PROSITE; PS00241; RECEPTOR_CYTOKINES_1; FALSE_NEG.
PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat; Signal.

CHAIN 1 19
DOMAIN 20 462
TRANSEM 21 357
DOMAIN 358 385
DOMAIN 386 462
DISULFID 47 92
DISULFID 117 128
DISULFID 162 173
CARBOHYD 32 32
CARBOHYD 85 85
CARBOHYD 150 150
CONFLICT 227 261
INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
POTENTIAL.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
POTENTIAL.
XPRWLKVSQMDPESNDPSYVLLQFELRYRFPWSKX ->
SLVGSFVSGKTLSPGQVTCNSSFDTLYGORT
(IN REF. 1).

SEQUENCE 462 AA; 50398 MW; A4D6064CEDC0537D CRC64;
Query Match 36.1%; Score 1361; DB 1; Length 462;
Best Local Similarity 55.6%; Pred. No. 2.44e-290;
Matches 188; Conservative 58; Mismatches 85; Indels 7; Gaps 4;

Db 1 MLAVGCTLLVALLAAPAVALVGLSCRALEVANGVTVSLPGATVTLICPGKEAAGNATHW 60
Oy 1 MLAVGCTLLVALLAAPAVALVGLSCRALEVANGVTVSLPGATVTLICPGKEAAGNATHW 60
Db 61 VY----SGSQSREWTGNTILVRAVQVNDTGHVLFDDHVLGTVPLIVDVPPEEPKLS 116
Oy 61 VLRKPAAGSHPSRWAGMGRLLRSVQLHDSGNSCYRAGRAGTAVHLLVDPPEEPOLS 120
Db 117 CFRKNPLVNAPFCWHPSPSTPTTKAVMFAKNTNTNGKSDFOVPCQYSOQLKFSCEVE 176
Oy 121 CFRKSPNSVVCVCGPRSTPILTKAVLLVRKFQNSPAE--DFQPCQYSOESQKSCOLA 179
Db 177 ILBGDKVHYHIVSLCVANSVSGSRSHNVVFSQSLKMWQVDPDPANILVVSAPGPRWLKYSWQ 236

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QY 180 VEGSSFYIVSMCVASSVGSFSTQTFQGGILQDPPANITVAVARNRWLSVTWQ 239
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
D 237 DPESMDPSYLLQFRLRYPVWKSXFTTVMPLQVAOQCVIHDALRGVHVQVRCKEED 296
    || ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 240 DPHSNWSFYRLRFLRAERSKFTTVMVKDLQHCVIDHAWGLRHVVQLRAQEFG 299
    || ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
D 297 IQGSKWSPEVTGTPWLAEPRTTPA-GIPGNPTQVSVE 333
    || ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 300 QGEWSEWSPAMGTPW-TESRPPARGGGGGGGGSVE 336
    || ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

RESULT 3
ID IL6A_MOUSE STANDARD; PRT; 460 AA.
AC P22272;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA).
GN IL6RA OR IL6R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C; TISSUE=SPLEEN;
RX MEDLINE; 90278354.
RA Sugita T., Totsuka T., Saito M., Yamasaki K., Taga T., Hirano T.,
RA Kishimoto T.
RT "Functional murine interleukin 6 receptor with the intracisternal A
RT particle gene product at its cytoplasmic domain. Its possible role in
RT plasmacytomagenesis."
RT J. Exp. Med. 171:2001-2009(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H; TISSUE=LIVER;
RA Florillo M.T., Ciliberto G., Dente L.;
RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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CC -----
DR EMBL; X51975; CAA36237.1; -.
DR EMBL; X53802; CAA37810.1; -.
DR PIR; JL0145; JL0145.
DR PIR; SI4543; SI4543.
DR HSP; P16471; IBP3.
DR MGD; MG1:105304; IL6RA.
DR PFAM; PF00041; fn3; 1.
DR PFAM; PF00047; 1g; 1.
DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
KW SIGNAL.
FT CHAIN 1 19 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
FT CHAIN 20 460
FT DOMAIN 21 357 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 358 385
FT DOMAIN 386 460 POTENTIAL.
FT DOMAIN 40 99 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 40 99 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 47 92 POTENTIAL.

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FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 162 173 BY SIMILARITY.
FT CARBOHYD 32 32 POTENTIAL.
FT CARBOHYD 55 55 POTENTIAL.
FT CARBOHYD 150 150 POTENTIAL.
FT CONFLICT 374 374 A -> R (IN REF. 2).
SQ SEQUENCE 460 AA; 50454 MW; F85C5906D08525C4 CRC64;

Query Match 35.0%; Score 1320; DB 1; Length 460;
Best Local Similarity 55.1%; Pred. No. 2.98e-280;
Matches 179; Conservative 58; Mismatches 82; Indels 6; Gaps 3;

Db 1 MLTGVCTLLVALLAAPAVALVLGSCRALEVANGTTSVTPGATVTLICPGKEAGNVTHW 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 MLAVGCALLAALLAAPGAALAPRCPAQVARGVLTSLPGDSVTLTCGVEPDNATVW 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D 61 VY----SGSQNREWTGNTGLVLRDVLQSDTGDCSLNDHLVGVTVPLLVDPVPEPKLS 116
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 VLKPAAGSHPSRWAGMGRLLRLSLVQLHDSGNSYCRAGRAGTGVHLLVDVPPPEPQLS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D 117 CFRKNPLVNAICEWRSPSTPTTKAVLFAKKTNTNGSKDFQVPCOYSQLKSESCOVE 176
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 CFRKPLSNVVCWGPSPSPSTTKAVLVRKFQNSPAB-DFQEPQCYSQESQKESCQLA 179
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D 177 ILEGDKVYHIVSLCVANSYSGKSSHNEAFHSLKMQVQDPPANLVSAIPGRPRWLKVSQ 236
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 VEGDSSFYIVSMCVASSVGSFSTQTFQGGILQDPPANITVAVARNRWLSVTWQ 239
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D 237 HPETWDPYSYLLQFRLRYPVWKSXFTTVMPLQVAOQCVIHDALRGVHVQVRCKEED 296
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 DPHSNWSFYRLRFLRAERSKFTTVMVKDLQHCVIDHAWGLRHVVQLRAQEFG 299
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D 297 LGQWSEWSPVGTGTPWLAEPRTTPA 321
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 300 QGEWSEWSPAMGTPW-TESRPPA 323
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
ID IL6_HUMAN STANDARD; PRT; 212 AA.
AC P05231.
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2)
DE (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR).
DE IL6 OR IFNB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE; 87065033.
RA Hirano T., Yasukawa K., Harada H., Taga T., Watanabe Y., Matsuda T.,
RA Kashiwamura S.-I., Nakajima K., Koyama K., Iwamatsu A., Tsunasawa S.,
RA Sakiyama F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.;
RT "Complementary DNA for a novel human interleukin (BSF-2) that induces
RT B lymphocytes to produce immunoglobulin.";
RT Nature 324:73-76(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88082664.
RA Yasukawa K., Hirano T., Watanabe Y., Muratani K., Matsuda T.,
RA Nakai S., Kishimoto T.;
RT "Structure and expression of human B cell stimulatory factor-2
RT (BSF-2/IL-6) gene.";
RL EMBO J. 6:2939-2945(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87067433.
RA May L.T., Helfgott D.C., Sehgal P.B.;
RT "Anti-beta-interferon antibodies inhibit the increased expression of
RT HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts:
RT structural studies of the beta 2 interferon involved.";

```

Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).
 [4] SEQUENCE FROM N.A.
 RN RP MEDLINE; 87053818.
 RX RA Zilberstein A., Ruggieri R., Korn J.H., Revel M.;
 RT "Structure and expression of cDNA and genes for human
 RT interferon-beta-2, a distinct species inducible by growth-stimulatory
 RT cytokines.";
 RL EMBL J. 5:2529-2537(1986).
 RN [5]
 RN RP SEQUENCE FROM N.A.
 RX RA MEDLINE; 88088768.
 RX RA Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
 RA Aarden L.A.;
 RT "Molecular cloning and expression of hybridoma growth factor in
 RT Escherichia coli.";
 RL J. Immunol. 139:4116-4121(1987).
 RN [6]
 RN RP SEQUENCE FROM N.A.
 RX RA MEDLINE; 89391958.
 RX RA Tonouchi N., Miwa K., Karasuyama H., Matsui H.;
 RT "Deletion of 3' untranslated region of human BSF-2 mRNA causes
 RT stabilization of the mRNA and high-level expression in mouse NIH3T3
 RT cells.";
 RL Biochem. Biophys. Res. Commun. 163:1056-1062(1989).
 RN [7]
 RN RP SEQUENCE FROM N.A.
 RX RA TISSUE-FIBROBLAST;
 RC MEDLINE; 87004683.
 RX RA Haegeman G., Content J., Volckaert G., Derynck R., Tavernier J.,
 RA Fiers W.;
 RT "Structural analysis of the sequence coding for an inducible 26-kDa
 RT protein in human fibroblasts.";
 RL Eur. J. Biochem. 159:625-632(1986).
 RN [8]
 RN RP SEQUENCE FROM N.A.
 RX RA MEDLINE; 89193317.
 RX RA Wong G., Wittek-Giannotti J., Hewick R., Clark S., Ogawa M.;
 RT "Interleukin 6: identification as a hematopoietic colony-stimulating
 RT factor.";
 RL Behring Inst. Mitt. 83:40-47(1988).
 RN [9]
 RN RP SEQUENCE FROM N.A.
 RX RA MEDLINE; 93178270.
 RX RA Chen Q.Y.;
 RT "Stable and efficient expression of human interleukin-6 cDNA in
 RT mammalian cells after gene transfer.";
 RL Chung-Hua Chung Liu Tsa Chih 14:340-344(1992).
 RN [10]
 RN RP SEQUENCE OF 30-63.
 RX RA MEDLINE; 88154445.
 RX RA van Damme J., van Beeumen J., Decock B., van Snick J., de Ley M.,
 RA Billiau A.;
 RT "Separation and comparison of two monokines with
 RT lymphocyte-activating factor activity: IL-1 beta and hybridoma growth
 RT factor (HGF). Identification of leukocyte-derived HGF as IL-6.";
 RL J. Immunol. 140:1534-1541(1988).
 RN [11]
 RN RP SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING 1ST DISULFIDE BOND.
 RX RA MEDLINE; 95154344.
 RX RA Breton J., la Fiura A., Bertolero F., Orsini G., Valsasina B.,
 RA Zilio R., de Filippis V., Polverino de Laureto P., Fontana A.;
 RT "Structure, stability and biological properties of a N-terminally
 RT truncated form of recombinant human interleukin-6 containing a single
 RT disulfide bond.";
 RL Eur. J. Biochem. 227:573-581(1995).
 RN [12]
 RN RP DISULFIDE BONDS.
 RX RA MEDLINE; 89286115.
 RX RA Glogston C.L., Boone T.C., Crandall B.C., Mendiaz E.A., Lu H.S.;
 RT "Disulfide structures of human interleukin-6 are similar to those of
 RT human granulocyte colony stimulating factor.";
 RL Arch. Biochem. Biophys. 272:144-151(1989).

[13] MUTAGENESIS.
 RN RP MEDLINE; 91243808.
 RX RA Luetticken C., Kruettgen A., Moeller C., Heinrich P.C., Rose-John S.;
 RT "Evidence for the importance of a positive charge and an
 RT alpha-helical structure of the C-terminus for biological activity of
 RT human IL-6.";
 RL FEBS Lett. 282:265-267(1991).
 RN [14]
 RN RP STRUCTURE BY NMR.
 RX RA MEDLINE; 96134845.
 RX RA Nishimura C., Watanabe A., Gouda H., Shimada I., Arata Y.;
 RT "Folding topologies of human interleukin-6 and its mutants as studied
 RT by NMR spectroscopy.";
 RL Biochemistry 35:273-281(1996).
 RN [15]
 RN RP STRUCTURE BY NMR.
 RX RA MEDLINE; 97303053.
 RX RA Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
 RA Cumming D.A.;
 RT "Solution structure of recombinant human interleukin-6.";
 RL J. Mol. Biol. 268:468-481(1997).
 RN [16]
 RN RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX RA MEDLINE; 97224126.
 RX RA Somers W., Stahl M., Seehra J.S.;
 RT "1.9-A crystal structure of interleukin 6: implications for a novel
 RT mode of receptor dimerization and signaling.";
 RL EMBL J. 16:989-997(1997).
 CC CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC CC
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 CC CC
 CC CC EMBL; X04430; CAA28026.1; -
 CC CC EMBL; M14584; AAA52728.1; -
 CC CC EMBL; X04602; CAA28268.1; -
 CC CC EMBL; Y00081; CAA68278.1; -
 CC CC EMBL; M18403; AAA52729.1; -
 CC CC EMBL; M29150; AAA59154.1; -
 CC CC EMBL; X04402; CAA27990.1; -
 CC CC EMBL; X04403; CAA27991.1; -
 CC CC EMBL; M54894; AAC41704.1; -
 CC CC EMBL; M56892; AAD13886.1; -
 CC CC EMBL; A09363; CAA00839.1; -
 CC CC PIR; A32648; IVHUB2.
 CC CC PIR; A25921; A25921.
 CC CC PDB; 1IL6; 04-FEB-98.
 CC CC PDB; 2IL6; 04-FEB-98.
 CC CC PDB; 1ALU; 03-JUN-98.
 CC CC MIM; 147620; -
 CC CC PFAM; PF00489; IL6; 1.
 CC CC PRINTS; PR00433; IL6GCSFPMGF.
 CC CC PRINTS; PR00434; INTERLEUKIN6.
 CC CC PROSITE; PS00254; INTERLEUKIN6; 1.
 CC CC Cytokine; Glycoprotein; Growth factor; Signal; 3D-structure.
 CC CC SIGNAL 1 29
 CC CC CHAIN 30 212 INTERLEUKIN-6.
 CC CC DISULFID 72 78
 CC CC DISULFID 101 111
 CC CC CARBOHYD 73 73
 CC CC MUTAGEN 173 173
 CC CC MUTAGEN 185 185
 CC CC A->V: ALMOST NO LOSS OF ACTIVITY.
 CC CC W->R: NO LOSS OF ACTIVITY.

FT MUTAGEN 204 204 S->P: 13% ACTIVITY.
FT MUTAGEN 210 210 R->K,E,Q,T,A,P: LOSS OF ACTIVITY.
FT MUTAGEN 212 212 M->T,N,S,R: LOSS OF ACTIVITY.
SQ SEQUENCE 212 AA; 23718 MW; 1FIEDIFE1B734079 CRC64;
Query Match 34.1%; Score 1287; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.84e-272;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 29 PVPVGGSDKDVAAAPHQPTSSERIDKQIRYILDGTSALRKETCNKSNMCSKEALAEN 88
QY 337 PVPVGGSDKDVAAAPHQPTSSERIDKQIRYILDGTSALRKETCNKSNMCSKEALAEN 396
Db 89 NNLPMKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEEQARAVQMSK 148
QY 397 NNLPMKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEEQARAVQMSK 456
Db 149 VLIQFLOKAKKALDAITTPDPTTNASLLTKLQAOQWLODMTHLLRSKFELQSSLA 208
QY 457 VLIQFLOKAKKALDAITTPDPTTNASLLTKLQAOQWLODMTHLLRSKFELQSSLA 516
Db 209 LRQM 212
QY 517 LRQM 520
RESULT 5
ID IL6_MACFA STANDARD; PRT; 212 AA.
AC P79341;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Macaca.
RN [1]
RP SEQUENCE FROM N.A.
RA Tatsumi M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC -----
CC EMBL; AB000554; BAA19148.1; -
DR HSP; P05231; 2116.
DR PFAM; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR PROSITE; PS00434; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78 POTENTIAL.
FT DISULFID 101 111 POTENTIAL.
FT CARBOHYD 73 73 POTENTIAL.
FT CARBOHYD 172 172 POTENTIAL.
SQ SEQUENCE 212 AA; 23654 MW; CFB173FCBF0B0389 CRC64;
Query Match 33.3%; Score 1257; DB 1; Length 212;

Best Local Similarity 96.7%; Pred. No. 8.91e-265;
Matches 178; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Db 29 PVLPGEDSKDVAAAPHQPTSSERIDKHRYILDGTSALRKETCNRSNMCSKEALAEN 88
QY 337 PVLPGEDSKDVAAAPHQPTSSERIDKHRYILDGTSALRKETCNRSNMCSKEALAEN 396
Db 89 NNLPMKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEEQARAVQMSK 148
QY 397 NNLPMKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEEQARAVQMSK 456
Db 149 VLIQFLOKAKKALDAITTPDPTTNASLLTKLQAOQWLODMTHLLRSKFELQSSLA 208
QY 457 VLIQFLOKAKKALDAITTPDPTTNASLLTKLQAOQWLODMTHLLRSKFELQSSLA 516
Db 209 LRQM 212
QY 517 LRQM 520
RESULT 6
ID IL6_MACMU STANDARD; PRT; 212 AA.
AC P51494;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Macaca.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RAC 2;
RX MEDLINE; 96003435.
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates".
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC -----
CC EMBL; L26028; AAA99978.1; -
DR HSP; P05231; 1ALU.
DR PFAM; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PROSITE; PS00434; INTERLEUKIN_6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78 POTENTIAL.
FT DISULFID 101 111 POTENTIAL.
FT CARBOHYD 73 73 POTENTIAL.
FT CARBOHYD 172 172 POTENTIAL.
SQ SEQUENCE 212 AA; 23728 MW; 4130DFE0CF0BCCAD CRC64;
Query Match 33.2%; Score 1251; DB 1; Length 212;
Best Local Similarity 95.7%; Pred. No. 2.64e-263;
Matches 176; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY	397	NLNLPMNAEKDGCFCQSGFNEETCLVKIITGLLEFVILEYLQNRFESSEQARAYQMSTK	456
Db	146	LLVQMLMKKYKSODEVTTPDPPTDTLSIQAILKAQDKWLKHHTTHILIRSLDFLOFSURA	205
QY	457	VLIQFLQKKAKNLDATTPDPTTNASULTKLQAQONQLQDMWTHILLRSFKREFLOSSURA	516
Db	206	VRIM	209
QY	517	LROM	520

RESULT	9
ID	IL6_ORCOR STANDARD; PRT; 205 AA.
AC	Q28747;
DT	15-FEB-2000 (Rel. 39, Created)
DT	15-FEB-2000 (Rel. 39, Last sequence update)
DT	15-FEB-2000 (Rel. 39, Last annotation update)
DE	INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
GN	IL6.
OS	Orcinus orca (Killer whale).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC	Orcinus.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE; 96163018.
RA	King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
RT	Stott J.L., Ferriock D.A.;
RT	"Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT	the harbor seal (<i>Phoca vitulina</i>), killer whale (<i>Orcinus orca</i>), and
RT	Southern sea otter (<i>Enhydra lutris nereis</i>).";
RL	Immunogenetics 43:190-195(1996).
CC	-I- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC	FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC	OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC	PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC	HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC	-I- SUBCELLULAR LOCATION: SECRETED.
CC	-I- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC	-----
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CC	ce or send an email to license@isb-sib.ch).
CC	-----

	EMBL; L46803; AAB01429.1;	-.
DR	HSP; P05231; IALU.	
DR	PFAM; PF00489; IL6; 1.	
DR	PROSITE; PS00254; INTERLEUKIN_6; 1.	
KW	Cytokine; Glycoprotein; Growth factor; Signal.	
FT	NON_TER .	1
FT	SIGNAL	<1
FT	CHAIN	21
FT	DISULFID	64
FT	DISULFID	93
FT	CARBOHYD	164
FT	N-LINKED (GLCNAC..)	(POTENTIAL).
SEQ	SEQUENCE	205 AA; 23266 MW; 6308F3A4579G0832 CRC64;
	Query Match	21.5%; Score 810; DB 1; Length 205;
	Best Local Similarity	60.7%;
	Matches	111; Conservative 36; Mismatches 35; Indels 1; Gaps 1;

[illegible]

Db	141	ALAAILKQKVKNPDEVTPDPPTNASLMNNLQSONDDMKNTKIIILILRSLENFTQFSLR	200
Qy	457	VLIQFLQKAKNLDAITTPDPTTNASLLTKLQAGNQLQDMMTHILRSKFEFLQSSLR	515
Db	201	AIR 203	
Ov	516	ALR 518	

RESULT	10				
ID	IL6_HORSE	STANDARD:	PRT;	208 AA.	
AC	Q95181; O19007;	O46568;			
DT	01-NOV-1997	(Rel. 35, Created)			
DT	15-JUL-1999	(Rel. 38, Last sequence update)			
DE	15-JUL-1999	(Rel. 38, Last annotation update)			
DE	INTERLEUKIN-6 PRECURSOR	(IL-6).			
GN	IL6.				
OS	Equus caballus (Horse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Perissodactylia; Equidae; Equus.				
[1]					
RP	SEQUENCE FROM N.A.				
RA	Swiderski C.E., Horohov D.W.;				
RL	Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.				
RN	[2].				
RP	SEQUENCE FROM N.A.				
RL	Leutenegger C.M., Huder J.B., von Rechenberg B., Akens M., Auer J.				
RP	Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.				
[3]					
RP	SEQUENCE FROM N.A.				

RT Cloning and expression of equine interleukin-6 "":
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY

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EMBL; U64794; AAB87703.1; -
DR DR PRINTS; PR00483; IL6GCSFMGF.
EMBL; AF005227; AAB62246.1; -
DR DR PROSITE; PR00434; INTERLEUKIN_6.
EMBL; AF011975; AAC04574.1; -
DR DR HSP; P05231; IALU
HSP; PF00489; IL6; 1
DR DR PRINTS; PR00433; IL6GCSFMGF.
DR DR PROSITE; PR00434; INTERLEUKIN_6.
DR DR PRINTS; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 27 POTENTIAL
CHAIN 28 208 INTERLEUKIN-6.
FT FT DISULFID 69 75 BY SIMILARITY.
FT FT DISULFID 98 108 BY SIMILARITY.
FT FT CARBOHYD 71 71 POTENTIAL.
FT FT CARBOHYD 184 184 POTENTIAL.
FT CONFLICT 4 5 LS -> FF (IN REF. 1).
FT CONFLICT 8 8 T -> A (IN REF. 3).
FT CONFLICT 137 137 I -> Y (IN REF. 2).
FT CONFLICT 205 205 V -> I (IN REF. 3).
SQ SEQUENCE 208 AA; 23325 MW; A62FAC23405BF66 CRC64;

Query Match	21.4%;	Score	806;	DB	1;	Length	208;
Best Local Similarity	59.2%;	Pred. No.	3.60e-155;				
Matches	109;	Conservative	42;	Mismatches	29;	Indels	

[illegible]

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RESULT      12
ID          IL6_CANFA         STANDARD;       PRT;        207 AA.
AC          PA1323;
DT          01-FEB-1995 (Rel. 31, Created)
DT          01-FEB-1995 (Rel. 31, Last sequence update)
DE          15-JUL-1998 (Rel. 36, Last annotation update)
DR          INTERLEUKIN-6 PRECURSOR (IL-6).
GN          IL6.
OS          Canis familiaris (Dog).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
[1]
SEQUENCE FROM N.A.
STRAIN=MONGREL;
MEDLINE;   94303924.
RA          Kukielka G.H., Youker K.A., Hawkins H.K., Perrard J.L.; Michael L.G., Ballantyne C.M., Smith C.W., Entman M.L.; "Regulation of ICAM-1 and IL-6 in myocardial ischemia: effect of reperfusion."; Ann. N.Y. Acad. Sci. 723:258-270(1994).
RL          -! FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC          -! SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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-----
EMBL; U12234; AAA83030.1; -.
DR          HSPB; P05231; 2IL6
DR          PFAM; PF00489; IL6; 1.
DR          PRINTS; PR00433; IL6GCSFMGF.
DR          PRINTS; PR00434; INTERLEUKIN_6.
DR          PROSITE; PS00254; INTERLEUKIN_6; 1.
CY          Cytokine; Glycoprotein; Growth factor; Signal.
FT          SIGNAL           ?    POTENTIAL.
FT          CHAIN            ?    207     INTERLEUKIN-6.
FT          DISULFID         67    73     BY SIMILARITY.
FT          DISULFID         96    106    BY SIMILARITY.
SQ          SEQUENCE      207 AA;  22945 MW;  45540154EA9COP50 CRC64;

Query Match              20.8%; Score 786; DB 1; Length 207;
Best Local Similarity 58.2%; Pred.No. 2.23e+150;
Matches 107; Conservative 37; Mismatches 40; Indels 0; Gaps 0;


Db                24 PGPLAGSKDDATSNSLPITSANKVPELIKYILGIKISALRKCDCRFNCKEDKSKEALAEN 83
Ov               337 PYVPGESSKDVAAPHROPIITSSRIDKOIRYLUDGISALRKETCNKNMCESSEKAELAEN 396

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Db 84 NLHLPKLEKDGCGFSGFNOETCLTRITTTGLVFEQHLNLQNNYEGDKENKSVHMSTK 143
QY 397 NLNLPRMAEKDGCFCGFGNEETCLVRIITGLLEFEVLEYLQNRFSSEBQARAVQMSTK 456
Db 144 ILVOMLKSVMKNODEVTTDPDPTDASLQALQSQDCVKKHTTHLLRLSLDFLQPSLRA 203
QY 457 VLIOFLQKRAKNLDAITTPDPTTNASLLTKLQAOQWLODMTHLLRSFKFELQSSLRA 516
Db 204 VRIM 207
QY 517 LRQM 520

RESULT 13
ID IL6_FELCA STANDARD; PRT; 208 AA.
AC P41683;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94162386.
RA Ohashi T., Matsumoto Y., Watari T., Goitsuka R., Tsujimoto H.,
RA Hasagawa A.;
RT "Molecular cloning of feline Interleukin-6 cDNA.";
RL J. Vet. Med. Sci. 55:941-944(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPHOCYTES;
RX MEDLINE; 94052249.
RA Bradley W.G., Gibbs C., Kraus L., Good R.A., Day N.K.;
RT "Molecular cloning and characterization of a cDNA encoding feline interleukin-6.";
RL Proc. Soc. Exp. Biol. Med. 204:301-305(1993).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
DR EMBL; L16914; AA16620.1; -
DR EMBL; D13227; BAA02507.1; -
DR HSP; P05231; 21L6.
DR PFAM; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PROSITE; PS00434; INTERLEUKIN_6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 208 INTERLEUKIN-6.
FT DISULFID 68 74 BY SIMILARITY.
FT DISULFID 97 107 BY SIMILARITY.
FT CONFLICT 2 2 T -> N (IN REF. 2).
FT CONFLICT 45 45 S -> P (IN REF. 2).
FT CONFLICT 133 133 E -> K (IN REF. 2).
FT CONFLICT 173 187 AKLSQSEWLRTTI -> LSCSHRVAAHNN (IN REF. 2).
FT CONFLICT 200 201 FS -> LR (IN REF. 2).
SQ SEQUENCE 208 AA; 23401 MW; 93B4456B2989CA4C CRC64;

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Query Match 20.8%; Score 786; DB 1; Length 208;
Best Local Similarity 57.8%; Pred. No. 2.23e-150;
Matches 100; Conservative 40; Mismatches 33; Indels 0; Gaps 0;

Db 36 ATNRLPLTSADKMEELIKYILKISALKKEMCDNYKNCKEDSKALAEENLNLPKLAEKD 95
QY 348 AAPHROPLOTSSRIDKQIRYILDIGISALRKETCNKSNKSSCKEALAEENLNLPKMAEKD 407
Db 96 GCFOSGFNOETCLTRITTTGLQEQIYLFLODKYEGDEENAKSVYVTSNVLQMLKPKGK 155
QY 408 GCFOSGFNEETCLVKIITGLLEFEVLEYLQNRFSSEBQARAVQMSTKVLIOFLQKRAK 467
Db 156 NODEVTIPVTEVGLQAKLSQSEWLRTTHLTLRLRLEDFLQFSLRVAVRM 208
QY 468 NLDAITTPDPTTNASLLTKLQAOQWLODMTHLLRSFKFELQSSLRALRQM 520

RESULT 14
ID IL6_BOVIN STANDARD; PRT; 208 AA.
AC P26892;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HOLSTEIN;
RX MEDLINE; 93076003.
RA Droogmans L., Cludts I., Cleuter Y., Kettmann R., Burny A.;
RT "Nucleotide sequence of bovine interleukin-6 cDNA.";
RL DNA Seq. 2:411-413(1992).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
DR EMBL; X57317; CAA40572.1; -
DR PIR; S22162; S22162.
DR HSP; P05231; 21L6.
DR PFAM; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PROSITE; PS00434; INTERLEUKIN_6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 208 INTERLEUKIN-6.
FT DISULFID 72 78 BY SIMILARITY.
FT DISULFID 101 111 BY SIMILARITY.
FT CARBOHYD 38 38 POTENTIAL.
SQ SEQUENCE 208 AA; 23758 MW; A0F000B9BA2EC341 CRC64;

Query Match 18.4%; Score 693; DB 1; Length 208;
Best Local Similarity 51.1%; Pred. No. 3.34e-128;
Matches 93; Conservative 46; Mismatches 39; Indels 4; Gaps 2;

Db 29 PGPIGEDFKNDTTPGRLLLTTPPEKTEALIKRMVDKISAMRKEICEKNDCESSKETLAEN 88

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QY	397	NLNLPMWAEKDCGFCQSGFNEETCLVKITIGLLEFEVLEYLQNRFESESEQARAVOMSTK	456
Db	149	TLIQILKEKIAGI--ITTP--ATNTDMLKMQSSNEWVKNAKVIIILRSLNFLOFSRA	204
QY	457	VLIFQLQKAKNLDATITPDPTTNASLITKLAQONQWLODMTTHILRSFKFLOSSRA	516
Db	205	IR 206	
QY	517	LR 518	

Search completed: Thu Aug 10 16:16:28 2000
Job time : 53 secs.

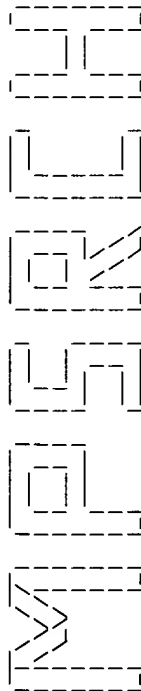
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RESULT 15
ID IL6_CAPHI STANDARD; PRT; 208 AA.
AC Q28319;
AD 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
DS IL6.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Caprinae; Capra.
OC [1]
SEQUENCE FROM N.A.
RX MEDLINE; 97392354.
RT Takakura H., Mori Y., Tatsumi M.;
RT "Molecular cloning of caprine IL-6 cDNA and its expression in insect
RT cells".
Int. Arch. Allergy Immunol. 113:409-416(1997).
-1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
-1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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EMBL; D86569; BAA13118.1; .
HSSP; P05231; 2IL6.
PEAM; PF00489; IL6; 1.
PRINTS; PR00433; IL6GCSFPMGF.
PRINTS; PR00434; INTERLEUKIN6.
PROSITE; PS00254; INTERLEUKIN_6; 1.
CYTOKINE; Glycoprotein; Growth factor; Signal.
SIGNAL 1 29 BY SIMILARITY.
CHAIN 30 208 INTERLEUKIN-6.
DISULFID 72 78 BY SIMILARITY.
DISULFID 101 111 BY SIMILARITY.
CARBOHYD 38 38 POTENTIAL.
SEQUENCE 208 AA; 23423 MW; E92E08BF3E3230A0 CRC64;

Query Match 18.1%; Score 683; DB 1; Length 208;
Best Local Similarity 51.1%; Pred. No. 7,87e-126;
Matches 93; Conservative 43; Mismatches 42; Indels 4; Gaps 2;

db 29 PGPLGEFDKNDTTPSRLLITTPKEKTEALIKHIVDKISAIRKEICKNDSCSKETLAEN 88
| | | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : |
337 PVPPEGSKDVAAPHRQPLTSSRIDKQIRYILDGISALRKETCNKSNMCESKKEALEN 396
| | | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : |
89 KILPKMEKGCDFOSGQNAICLLIKTWAGLLEYQIYLDLFONEFGNETVMEQSSIR 148
| : | | | | | | | | | | | | | | | : | | | : | | | : | | | : |

```



(TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Aug 10 16:13:42 2000; MasPar time 26.82 Seconds
Tabular output not generated. 914.465 Million cell updates/sec

Title: >US-09-142-471-4
Description: (1-520) from US09142471.pep
Perfect Score: 3771
Sequence: 1 MNAVGCALLAALLAAGPAAAL.....LILSPKFEFLQSSLRALRQM 520

Scoring table: PAM 150
Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir64
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 49.906; Variance 97.591; scale 0.511

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	2398	63.6	468	1	A41242	interleukin-6 recepto	0.00e+00
2	1320	35.0	440	2	JL0144	interleukin-6 recepto	7.38e-244
3	1320	35.0	460	2	JL0145	interleukin-6 recepto	7.38e-244
4	1287	34.1	212	1	IVH0B2	interleukin-6 precurs	8.47e-237
5	1095	29.0	462	1	A37986	interleukin-6 recepto	7.11e-196
6	806	21.4	208	2	T09216	interleukin-6 precurs	6.02e-135
7	801	21.2	212	2	I46590	interleukin 6 - pig	6.67e-134
8	801	21.2	212	2	I46521	prointerleukin 6 - pi	6.67e-134
9	693	18.4	208	1	A56610	interleukin-6 precurs	1.87e-111
10	680	18.0	207	2	I46084	interleukin 6 - cat	9.08e-109
11	679	18.0	208	1	S29549	interleukin-6 - sheep	1.46e-108
12	560	14.9	211	1	ICWS6	interleukin-6 precurs	3.53e-84
13	558	14.8	211	1	A34247	interleukin-6 precurs	9.01e-84
14	409	10.8	372	2	I58141	ciliary neurotrophic	5.66e-54
15	408	10.8	372	1	UHHUCN	ciliary neurotrophic	8.89e-54
16	406	10.8	432	2	I48343	interleukin-11 recept	2.19e-53
17	397	10.5	422	2	I37891	interleukin-11 recept	1.27e-51
18	373	9.9	362	2	S60614	growth promoting acti	5.92e-47
19	212	5.6	831	2	JQ1655	prolactin receptor pr	3.65e-17
20	179	4.7	201	2	A42247	myelomonocytic growth	1.30e-11
21	179	4.7	581	2	I45971	prolactin receptor -	1.30e-11
22	172	4.6	830	2	I50455	prolactin receptor -	1.77e-10
23	165	4.4	630	2	I51086	prolactin receptor -	2.33e-09

ALIGNMENTS

RESULT 1

ENTRY Interleukin-6 receptor precursor - human
TITLE Interleukin-6 receptor, soluble form
CONTAINS #formal_name Homo sapiens #common_name man
ORGANISM 27-Mar-1992 #sequence_revision 02-Dec-1994 #text_change
DATE 22-Jun-1999

ACCESSIONS A41242; J00080; S17468; A61459; S14621
REFERENCE A41242
#authors Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, T.; Hirano, T.; Kishimoto, T.
#journal Science (1988) 241:825-828
#title Cloning and expression of the human interleukin-6 (BSP-2/IFNbeta 2) receptor.
#cross-references MIM:88305347

#accession A41242
#molecule_type mRNA
#residues 1-468 #label YAM
#cross-references GB:M20566; NID:g186346; PID:g307062

REFERENCE J00080
#authors Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, T.; Hirano, T.; Kishimoto, T.
#journal Proc. Jpn. Acad. (1988) 64:209-211
#title Molecular structure of interleukin 6 receptor.

#accession J00080
#molecule_type mRNA
#residues 1-468 #label YA2

REFERENCE S17468
#authors Schooltink, H.; Stoyan, T.; Lenz, D.; Schmitz, H.; Hirano, T.; Kishimoto, T.; Heinrich, P.C.; Rose-John, S.
#journal Biochem. J. (1991) 277:659-664
#title Structural and functional studies on the human hepatic interleukin-6 receptor. Molecular cloning and overexpression in HepG2 cells.

#cross-references MIM:91336983

#accession S17468

#molecule_type mRNA

#residues 1-468 #label SCH

#cross-references EMBL:X56298; NID:g32580; PIDN:CAA1231.1; PID:g32581

#experimental_source Hepatoma cell line HepG2

REFERENCE A61459

#authors Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M.

#journal J. Exp. Med. (1989) 170:1409-1414

#title Soluble cytokine receptors are present in normal human urine.

#cross-references MIM:90010793

#accession A61459

#molecule_type protein

glycoprotein 130 - mo 8.60e-08
prolactin receptor 2 2.49e-07
prolactin receptor - 8.05e-06
prolactin receptor lo 4.05e-06
erythropoietin recept 3.13e-05
prolactin receptor pr 1.59e-05
prolactin receptor Nb 1.59e-05
prolactin receptor 2 1.59e-05
lactogen receptor 1 - 1.59e-05
membrane glycoprotein 1.13e-05
interleukin-6 signal 2.24e-05
prolactin receptor pr 4.39e-05
prolactin receptor pr 4.39e-05
prolactin receptor, l 4.39e-05
LMO protein - fruit f 8.57e-04
interleukin 12b precu 1.18e-03
leptin receptor, Ob-R 6.20e-04
leptin receptor precu 6.20e-04
leptin receptor, isof 6.20e-04
leptin receptor, Ob-R 6.20e-04
leptin receptor (vari 3.10e-03
leptin receptor (vari 3.10e-03

```

##residues      20-49 ##label NOV
COMMENT      Through this receptor, interleukin-6 induces proliferation,
              activation, and differentiation of various cell types.
COMMENT      This growth factor receptor does not have a tyrosine kinase domain.
GENETICS
#gene        GDB:IL6R
#map_position 1q21-lq21
#cross-references GDB:127966; OMIM:147880
CLASSIFICATION #superfamily ciliary neurotrophic factor receptor; cytokine
               receptor homology; immunoglobulin homology
KEYWORDS      acute phase; cytokine receptor; glycoprotein; transmembrane
               protein
FEATURE
1-19          #domain signal sequence #status predicted #label SIG\
20-468        #product interleukin-6 receptor #status predicted #label
               MAT\
20-363        #domain extracellular #status predicted #label EXT\
40-98         #domain immunoglobulin homology #label IMM2\
121-309       #domain cytokine receptor homology #label CRS\
364-386       #domain transmembrane #status predicted #label TM\
387-468       #domain intracellular #status predicted #label INT\
47-96         #disulfide bonds #status predicted\
55,93,221,245,350 #binding_site carbohydrate (Asn) (covalent) #status
               predicted\
SUMMARY       #length 468 #molecular-weight 51547 #checksum 4661
               63.6%; Score 2398; DB 1; Length 468;
Query Match   Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1  MLAVGCALLAALLAAGAALAPRCPCPAQEVARGVLTSLPGDSVLTLCGVEPDNATVHW 60
QY 1  MLAVGCALLAALLAAGAALAPRCPCPAQEVARGVLTSLPGDSVLTLCGVEPDNATVHW 60

Db 61  VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120
QY 61  VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

Db 121  CFRKSPLSNVVCEWGPSTSLTKAVLLVRKFQNSPAEDFQPCQYSOESQKFSQCLAV 180
QY 121  CFRKSPLSNVVCEWGPSTSLTKAVLLVRKFQNSPAEDFQPCQYSOESQKFSQCLAV 180

Db 181  PEGDSSFYIVSMCVASSVSGSFSTQTFQGGIILQDPPANITVAVARNRWLSVTWQD 240
QY 181  PEGDSSFYIVSMCVASSVSGSFSTQTFQGGIILQDPPANITVAVARNRWLSVTWQD 240

Db 241  PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDWAGSLRHVVOLRAQEFGQ 300
QY 241  PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDWAGSLRHVVOLRAQEFGQ 300

Db 301  GEWSEWSPAMGTPWTSRSPPA 323
QY 301  GEWSEWSPAMGTPWTSRSPPA 323

RESULT 2
ENTRY   #type complete
TITLE   interleukin-6 receptor precursor (clone lambda p1) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE    31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change

ACCESSIONS
REFERENCE #authors
          Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.;
          Hirano, T.; Kishimoto, T.
#journal J. Exp. Med. (1990) 171:2001-2009
#title   Functional murine interleukin 6 receptor with the
          intracisternal a particle gene product at its cytoplasmic
          domain: its possible role in plasmacytomagenesis.
#cross-references MIM:90278354
#accession JLO144
#status    #molecule_type mRNA
##residues 1-373, 'R', 375-460 ##label FTO
##cross-references EMBL:X53802; NID:952692; NID:CAA37810.1; PID:952693
CLASSIFICATION #superfamily ciliary neurotrophic factor receptor; cytokine

```

```

##residues      1-440 ##label SUG
#cross-references GDB:X51976; NID:953548; PIDN:CAA36238.1; PID:g53549
CLASSIFICATION #superfamily ciliary neurotrophic factor receptor; cytokine
               receptor homology; immunoglobulin homology
               cytokine receptor; transmembrane protein
KEYWORDS
FEATURE
1-19          #domain signal sequence #status predicted #label SIG\
20-440        #product interleukin-6 receptor #status predicted #label
               MAT\
117-306       #domain cytokine receptor homology #label CRS\
358-385       #domain transmembrane #status predicted #label TRA
SUMMARY       #length 440 #molecular-weight 47901 #checksum 5876
               35.0%; Score 1320; DB 2; Length 440;
Query Match   Best Local Similarity 55.1%; Pred. No. 7.38e-244;
Matches 179; Conservative 58; Mismatches 82; Indels 6; Gaps 3;

Db 1  MLTVGCTLLVALLAALPAVALVLSGCRALVANGVTVSLPGATVTLICPGKAAGNVIHW 60
QY 1  MLAVGCALLAALLAAGAALAPRCPCPAQEVARGVLTSLPGDSVLTLCGVEPDNATVHW 60

Db 61  VY----SGSQNRWTTGNTILVLDVQLSDTGDYLCSLNDHLVGTVPVLLVDVPPPEPKLS 116
QY 61  VLRKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

Db 117  CFRKNPLVNAICEWRSPSTPSTTKAVLFAKKINTNGKSDFOVCOYSQOLKSFQCOVE 176
QY 121  CFRKSPLSNVVCEWGPSTSLTKAVLLVRKFQNSPAE-DFQPCQYSOESQKFSQCLA 179

Db 177  ILEGDKYVHVIVSLCVANSVSGSKSHNEAFHSLKMPDPANLVSAIPGRPLWKYSWQ 236
QY 180  VPEGDSSFYIVSMCVASSVSGSKFTQTFQGGIILQDPPANITVAVARNRWLSVTWQ 239

Db 237  HPETWDSYLLQQLRYRPVNSKEFTVLLLPVAYOCVTHDALRGVHVQVVGKELD 296
QY 240  DPHWNSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDWAGSLRHVVOLRAQEFG 299

Db 297  LGOWSEWSPVETGTPWIAEPRTTPA 321
QY 300  QGEWSEWSPAMGTPW-TESRSPPA 323

```

```

RESULT 3
ENTRY   #type complete
TITLE   interleukin-6 receptor precursor (clone lambda 301) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE    31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change

ACCESSIONS
REFERENCE #authors
          Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.;
          Hirano, T.; Kishimoto, T.
#journal J. Exp. Med. (1990) 171:2001-2009
#title   Functional murine interleukin 6 receptor with the
          intracisternal a particle gene product at its cytoplasmic
          domain: its possible role in plasmacytomagenesis.
#cross-references MIM:90278354
#accession JLO145; SI4543
#status    #molecule_type mRNA
##residues 1-460 ##label SUG
##cross-references GDB:X51975; NID:949725; PIDN:CAA36237.1; PID:949726
REFERENCE #experimental_source clone lambda 301
          SI4543
#authors  Fiorillo, M.T.; Ciliberto, G.; Dente, L.
#submission submitted to the EMBL Data Library, July 1990
#description Cloning and expression of murine IL-6 receptor.
#accession SI4543
#status    #molecule_type mRNA
##residues 1-373, 'R', 375-460 ##label FTO
##cross-references EMBL:X53802; NID:952692; NID:CAA37810.1; PID:952693
CLASSIFICATION #superfamily ciliary neurotrophic factor receptor; cytokine

```



```

##residues 1-212 ##label BRA
##cross-references GB:M18403; NID:g184631; PIDN:AAAS2729.1; PID:g306911
REFERENCE A92816
#authors Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De
Ley, M.; Billiau, A.
#journal J. Immunol. 140:1534-1541
#title Separation and comparison of two monokines with
lymphocyte-activating factor activity: IL-1-beta and
hybridoma growth factor (HGF). Identification of
leukocyte-derived HGF as IL-6.
#cross-references MUID:88154445
#accession A27601
##molecule_type protein
##residues 28-51,'X',53-57,'X',59,'X',61 ##label VAN1
#accession B27601
##molecule_type protein
##residues 30-56,'XX',59-61,'X',63 ##label VA2
REFERENCE A60400
#authors Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
#journal J. Immunol. (1990) 144:1808-1816
#title The human lung fibroblast cell line, MRC-5, produces multiple
factors involved with megakaryocytopoiesis.
#cross-references MUID:90171574
#accession A60400
##molecule_type protein
##residues 30-43 ##label YAM
REFERENCE A29085
#authors Hirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.;
Takatsuki, F.; Shimizu, M.; Murashima, A.; Tsunasawa, S.;
Sakiyama, F.; Kishimoto, T.
#journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:228-231
#title Human beta-cell differentiation factor defined by an
anti-peptide antibody and its possible role in autoantibody
production.
#cross-references MUID:87092370
#accession A29085
##molecule_type protein
##residues 29-42 ##label HIR2
REFERENCE A61159
#authors Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.;
Hara, T.; Ishikawa, H.; Arimura, H.; Konno, K.
#journal Anticancer Res. (1991) 11:961-968
#title Purification and characterization of human fibroblast derived
differentiation inducing factor for human monoblastic
leukemia cells identical to interleukin-6.
#cross-references MUID:91290785
#accession A61159
##molecule_type protein
##residues 30-42 ##label NOD
##experimental_source fibroblast
REFERENCE A61462
#authors Ming, J.E.; Cernetti, C.; Steinman, R.M.; Granelli-Piperno,
A.
#journal J. Mol. Cell. Immunol. (1989) 4:203-212
#title Interleukin 6 is the principal cytolytic T lymphocyte
differentiation factor for thymocytes in human leukocyte
conditioned medium.
#cross-references MUID:90121567
#accession A61462
##molecule_type protein
##residues 28-48 ##label MIN
##experimental_source leukocyte-conditioned medium
REFERENCE A48419
#authors May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriskie, J.B.; Sehgal,
P.B.
#journal Cytokine (1991) 3:204-211
#title Marked cell-type-specific differences in glycosylation of
human interleukin-6.
#cross-references MUID:91355644
#accession A48419
##molecule_type protein
##residues 30-37,'X',39-40 ##label MAY2
##experimental_source FS-4 fibroblasts

```

```

##note sequence extracted from NCBI backbone
##note this 28-30K form contained both N-linked and O-linked
carbohydrate; a 25K form containing only N-linked
carbohydrate was also found
#accession C48419
##molecule_type protein
##residues 28-40 ##label MAY3
##experimental_source FS-4 fibroblasts
##note sequence extracted from NCBI backbone (NCBIP:63787)
##note this 23-25K form contained O-linked but not N-linked
carbohydrate
REFERENCE JX0305
#authors Orita, T.; Oheda, M.; Hasegawa, M.; Kuboniwa, H.; Esaki, K.;
Ochi, N.
#journal J. Biochem. (1994) 115:345-350
#title Polypeptide and carbohydrate structure of recombinant human
interleukin-6 produced in chinese hamster ovary cells.
#cross-references MUID:94266765
#contents annotation; modified sites in recombinant protein from CHO
cells
REFERENCE S04981
...
Note: remainder of annotations omitted.
Query Match 34.1%; Score 1287; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 8,47e-237;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 29 PVPGEQSKDVAAPROPLTSSRIDKQIRYLDIGISALRKETCNKSNMCSSEKALAE 88
|||||
Qy 337 PVPGEQSKDVAAPROPLTSSRIDKQIRYLDIGISALRKETCNKSNMCSSEKALAE 396
|||||
Db 89 NLNLPKAEKDCGQSGFNEETCLVKIITGLLEFEVLYLQNFESSEQARAVQMSK 148
|||||
Qy 397 NLNLPKAEKDCGQSGFNEETCLVKIITGLLEFEVLYLQNFESSEQARAVQMSK 456
|||||
Db 149 VLIQFLOKAKNLDATITPDPPTNASLTKLQAOQNOWLQDMMTHILRSFEFLQSSLR 208
|||||
Qy 457 VLIQFLOKAKNLDATITPDPPTNASLTKLQAOQNOWLQDMMTHILRSFEFLQSSLR 516
|||||
Db 209 LRQM 212
||||
Qy 517 LRQM 520
||||
RESULT 5
ENTRY A37986 #type complete
TITLE interleukin-6 receptor precursor - rat
ALTERNATE_NAMES IL-6 receptor
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
22-Jun-1999
ACCESSIONS A37986
REFERENCE A37986
#authors Baumann, M.; Baumann, H.; Fey, G.H.
#journal J. Biol. Chem. (1990) 265:19853-19862
#title Molecular cloning, characterization and functional expression
of the rat liver interleukin 6 receptor.
#cross-references MUID:91060602
#accession A37986
##molecule_type mRNA
##residues 1-462 ##label BAU
##cross-references GB:M58587; GB:J05668; NID:g204921; PIDN:AAA41431.1;
PID:g204922
COMMENT After binding IL-6, this chain associates with a 130K glycoprotein
that is essential for transmembrane signaling.
CLASSIFICATION #superfamily ciliary neurotrophic factor receptor; cytokine
receptor homology; immunoglobulin homology
KEYWORDS acute phase; cytokine receptor; transmembrane protein
FEATURE 1-19 #domain signal sequence #status predicted #label SIG\
20-462 #product interleukin-6 receptor #status predicted #label
MAY\

```


20-362 #domain extracellular #status predicted #label EXT\
40-94 #domain immunoglobulin homology #label IMM\
117-306 #domain cytokine receptor homology #label CRS\
363-385 #domain transmembrane #status predicted #label TMN\
386-462 #domain intracellular #status predicted #label INT\
47-92 #disulfide_bonds #status predicted
SUMMARY #length 462 #molecular-weight 49560 #checksum 9669

Query Match 29.0%; Score 1095; DB 1; Length 462;
Best Local Similarity 50.6%; Pred. No. 7.11e-196;
Matches 172; Conservative 58; Mismatches 99; Indels 11; Gaps 7;

Db 1 MLAVGCTLLVALLAAPAVALVGLSCRALEVANGTVTSLPGATVTLICPGKEAAGNATIHW 60
QY 1 MLAVGCALLAALLAAPGAALAPRCAPAQEVARGVLTSLPGDSVTLCPCGVEPDNATVHW 60

Db 61 VY----SGSQSREWTGTVTLVLRVQVNDTGHYLCFLDDHLVGTVPLLVDVPPPEPKLS 116
QY 61 VLRKPAAGSHPRGWRAGMRLLRSVQLHSDGNSYCYRAGRAGTAVHLLVDVPPPEPKLS 120

Db 117 CFRKNPLVNAFCWEHPSSPTTKAVMFAKKINTTNGKSDFOVPCOYSQOLKSFSCVE 176
QY 121 CERKSPLSNVCEWGPSPSTLTKAVLLVRKFQNSPAE-DQEPQOYQSQESKQFSCQLA 179

Db 177 ILEGDKVYHIVSLCVANSVGRSSHNVPFSLKMVQDPPANLVSAIPGSLVGRSKVGK 236
QY 180 VPEGDSSEFIVSMCVASSVSGSKFSTQTQGGGILQDPPANITVTAVARNPR-WLSVTW 238

Db 237 TILSPGTQVITCCNSSFDTLQGR--TFVWPLOYAQHOCVHDALRGVHVQVGRKEE 294
QY 239 Q-DPHSWNSSFYRLRFLRYRAERSKFTTWMVKDLQHCYVHDWSGLRHVVQLRAQEE 297

Db 295 FDIGOWSKWSPVETGPPVLAEPRTTPA-GIPGNPTQVSVE 333
QY 298 FQGEWSEWSPAMGTPW-TESRPPARGGGGGGGSGVE 336

RESULT 6 #type complete
ENTRY interleukin-6 precursor - horse
TITLE #formal_name Equus caballus #common_name domestic horse
ORGANISM 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change
DATE 23-Jul-1999

ACCESSIONS T09216
REFERENCE Z16613
#authors Swiderski, C.E.; Horohov, D.W.
#submission submitted to the EMBL Data Library, July 1996
#accession T09216
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-208 #label SWI
#cross-references EMBL:U64794; NID:g2654387; PID:g2654388

GENETICS IL-6
#gene
#superfamily interleukin-6
#length 208 #molecular-weight 23419 #checksum 3370

Query Match 21.4%; Score 806; DB 2; Length 208;
Best Local Similarity 59.2%; Pred. No. 6.02e-135;
Matches 109; Conservative 42; Mismatches 29; Indels 4; Gaps 3;

Db 29 PLPLGSD--E-TSNGPLLTADKTKQHLYKILGKTSALKNMCNFKSCNSKEVLAEN 85
QY 337 PVPVPGSDSKVAAPHRQPLTSSRIDKQIRYILDGISALRKETCNKSNMCESKEALAE 396

Db 86 NLNLPMKAEKDCFGSGFNQETLMKITTLGSEFQIYLEYLQNEFKGKENTKTMQISTK 145
QY 397 NLNLPMKAEKDCFGSGFNEETCLVKIITGLLEFVLEYLQNRFFESSEQARAVQMSTK 456

Db 146 VLVIQILMQKKNPE-VTTPDPPTAKSLAKHSQNEWLNKNTTHLILRSLEDFLOQSLRA 204
QY 457 VLTIQFLQKAKNLDAITTPDPTNASLLTKLQAQNWQLQDMTTHLILRSFKEFLQSLRA 516

Db. 205 VRIM 208
QY 517 LRQM 520

RESULT 7 #type complete
ENTRY interleukin 6 - pig
TITLE #formal_name Sus scrofa domestica #common_name domestic pig
ORGANISM 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
DATE 16-Jul-1999

ACCESSIONS I46590
REFERENCE I46590
#authors Mathialagan, N.; Bixby, J.; Roberts, M.R.
#journal Mol. Reprod. Dev. (1992) 32:324-330
#title Expression of interleukin-6 in porcine, ovine, and bovine preimplantation conceptuses.
#cross-references MUID:92360284
#accession I46590
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-212 #label MAT
#cross-references GB:M80258; NID:g164514; PIDN:AAC27127.1; PID:g164515

GENETICS IL-6
#gene
#superfamily interleukin-6
#length 212 #molecular-weight 23952 #checksum 759

CLASSIFICATION
SUMMARY

Query Match 21.2%; Score 801; DB 2; Length 212;
Best Local Similarity 59.8%; Pred. No. 6.67e-134;
Matches 107; Conservative 37; Mismatches 35; Indels 0; Gaps 0;

Db 34 EDAGKDATSDKMLFTSPDKTEELIKYILGKISAMRCKEYKCKENSKVLAENNLNP 93
QY 342 EDSKDVAAPHRQPLTSSRIDKQIRYILDGISALRKETCNKSNMCESKEALAE 401

Db 94 KMAEKDGCFCGSGFNQETCLMRITTLGVEFOIYLDYLOKYEYKNGVNAEAVQISTKALIQ 153
QY 402 KMAEKDGCFCGSGFNEETCLVKIITGLLEFVLEYLQNRFFESSEQARAVQMSTKVLQ 461

Db 154 LRQKGNPKATPNTPTNAGLLDKLQSQNEWMKNTKIILRSLEDFLOFSURAIM 212
QY 462 LQKAKNLDAITTPDPTNASLLTKLQAQNWQLQDMTTHLILRSFKEFLQSLRALQM 520

RESULT 8 #type complete
ENTRY prointerleukin 6 - pig
TITLE #formal_name Sus scrofa domestica #common_name domestic pig
ORGANISM 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
DATE 16-Jul-1999

ACCESSIONS I46621
REFERENCE I46621
#authors Richards, C.; Saklatva, J.
#journal Cytokine (1991) 3:269-276
#title Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and Expression of mRNA in Synovial Fibroblasts In Vitro.
#cross-references MUID:91338547
#accession I46621
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-212 #label RIC
#cross-references GB:M86722; NID:g164624; PIDN:AAC37333.1; PID:g164625

GENETICS IL6
#gene
#superfamily interleukin-6
#length 212 #molecular-weight 23880 #checksum 819

CLASSIFICATION
SUMMARY

Query Match 21.2%; Score 801; DB 2; Length 212;
Best Local Similarity 59.8%; Pred. No. 6.67e-134;
Matches 107; Conservative 37; Mismatches 35; Indels 0; Gaps 0;


```
Db 34 EDAGDQATSKMLFTSPDKTEELIKYILGKISAMRKCEKYEKCNSEKVEIAENNLNP 93
||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : :
QY 342 EDSKDVAAAPHRQPLASSERIDQIRYILDGISALRKETCNKSNMCESSKEALAENNLNP 401
||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : :
Db 94 KMAEKDGCQSGFQNETCLMRITTTGLVFEQIYLDYLOKYESKNKNVAVQISKALITOT 153
||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : :
QY 402 KMAEKDGCQSGFQNETCLVKITGLLEFEVYLEYQNRFFESSEQARAVQMSTKVLIOF 461
||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : :
Db 154 LRQKGNPKDATTPTNTNAGLLDKLOSNEHMKTKIILILRSLEDFLOSLRAIRM 212
||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : :
QY 462 LQKAKNLDAITTPDTTNASLLTKLQAOQNLQDM-TTHILRSKFELQSSLRALQOM 520
||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : :

RESULT 9
ENTRY A56610 #type complete
TITLE Interleukin-6 precursor - bovine
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
ACCESSIONS A56610; S22162
REFERENCE A56610
#authors Droogmans, L.; Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.
#journal DNA Seq. (1992) 2:411-413
#title Nucleotide sequence of bovine interleukin-6 cDNA.
#cross-references MUID:93076003
#accession A56610
#status preliminary
#molecule_type mRNA
#residues 1-208 #label DRO
#cross-references EMBL:X57317; NID:g2193; PIDN:CAA40572.1; PID:g2194
#experimental_source BLV induced B cell-lymphosarcoma
#note sequence extracted from NCBI backbone (NCBIP:118917)
CLASSIFICATION #superfamily interleukin-6
KEYWORDS cytokine
SUMMARY #length 208 #molecular-weight 23758 #checksum 8010

Query Match 18.4%; Score 693; DB 1; Length 208;
Best Local Similarity 51.1%; Pred. No. 1.87e-111;
Matches 93; Conservative 46; Mismatches 39; Indels 4; Gaps 2;

Db 29 PGPLEGDKNDTPGRLLTTPKTEALIKRMVDKISAMRKEICEKNDCESSKETLAEN 88
| | | | : : : : | | | | : : : : | | | | : : : : | | | | : : : :
QY 337 PVPGEDSKDVAAPHRQPLTSSERIDQIRYILDGISALRKETCNKSNMCESSKEALAEN 396
| | | | : : : : | | | | : : : : | | | | : : : : | | | | : : : :
Db 89 KLNLPKMEKDCGCGSGFNQAICTRTAGLLEQIYLDYLONEYEGNQENVRLKNIIR 148
: | | | | | | | | : | | : | | : | | : | | : | | : | | : | | :
QY 397 NLNLPKMAEKDGCQSGFQNETCLVKITGLLEFEVYLEYQNRFFESSEQARAVQMSTK 456
| | | | : : : : | | | | : : : : | | | | : : : : | | | | : : : :
Db 149 TLIQILKOKIADL--ITTP--ATNTDLEKMOSSNEWKNKAKIILILRNLENFLQSLRA 204
||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : :
QY 457 VLIQFLQKAKNLDAITTPDTTNASLLTKLQAOQNLQDM-TTHILRSKFELQSSLR 516
||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : :
Db 205 IR 206
QY 517 LR 518

RESULT 10
ENTRY I46084 #type complete
TITLE Interleukin 6 - cat
ORGANISM #formal_name Felis silvestris catus #common_name domestic cat
DATE 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change
ACCESSIONS I46084
REFERENCE I46084
#authors Bradley, W.G.; Gibbs, C.; Kraus, L.; Good, R.A.; Day, N.K.
#journal Proc. Soc. Exp. Biol. Med. (1993) 204:301-305
#title Molecular cloning and characterization of a cDNA encoding feline interleukin-6.
#cross-references MUID:94052249
#accession I46084
#status preliminary; translated from GB/EMBL/DBJ
```

```
##molecule_type mRNA
##residues 1-207 ##label BRA
##cross-references GB:LI6914; NID:9438519; PIDN:AAAL6620.1; PID:9438520
CLASSIFICATION #superfamily interleukin-6
SUMMARY #length 207 #molecular-weight 23212 #checksum 9069

Query Match 18.0%; Score 680; DB 2; Length 207;
Best Local Similarity 52.3%; Pred. No. 9.08e-109;
Matches 91; Conservative 41; Mismatches 39; Indels 3; Gaps 2;

Db 36 ATSNRLPLTPADKMEELIKYILGKISALKKEMCDNKNKCEDSKALAENNLNPKLAEKD 95
| : : | | | : : : : | : : | | | : : : | : : | | | : : : | : : | | |
QY 348 AAPHRQPLTSSERIDQIRYILDGISALRKETCNKSNMCESSKEALAENNLNPKMAEKD 407
| : : | | | : : : : | : : | | | : : : | : : | | | : : : | : : | | |

Db 96 GCFOSGFNQETCLRTITGLOEFOIYLFLODKYEGDKENAKSVYTSNVLLQMLKRKGK 155
| | | | : : : : | | | | : : : : | | | | : : : : | | | | : : : :
QY 408 GCFOSGFNEETCLVKIITGLLEFEVYLEYQNRFFESSEQARAVQMSTKVLIOFLQKAK 467
| | | | : : : : | | | | : : : : | | | | : : : : | | | | : : : :

Db 156 NODEVTIPVPTVEVGL--QLSCSHRRVAEHNHLLTLRLLEDFLQRLRAVRIM 207
| | : | | | : : : : | : : : : | : : : : | : : : : | : : : :
QY 468 NLDAITTPDTTNASLLTKLQAOQNLQDM-TTHILRSKFELQSSLRALQOM 520
||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : :

RESULT 11
ENTRY S29549 #type complete
TITLE Interleukin-6 - sheep
ORGANISM #formal_name Ovis orientalis aries, Ovis ammon aries
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
ACCESSIONS S29549
REFERENCE S29549
#authors Ebrahimi, B.
#submission submitted to the EMBL Data Library, October 1992
#accession S29549
#status preliminary
#molecule_type mRNA
#residues 1-208 ##label EBR
#cross-references EMBL:X68723
CLASSIFICATION #superfamily interleukin-6
SUMMARY #length 208 #molecular-weight 23526 #checksum 7927

Query Match 18.0%; Score 679; DB 1; Length 208;
Best Local Similarity 50.5%; Pred. No. 1.46e-108;
Matches 92; Conservative 43; Mismatches 43; Indels 4; Gaps 2;

Db 29 PGPLEGDKNDTPPSRLTTPKTEALIKHIYDKISAIRKEICEKNDCEKSNKETLAEN 88
| | | | : : : : | | | | : : : : | | | | : : : : | | | | : : : :
QY 337 PVPGEDSKDVAAPHRQPLTSSERIDQIRYILDGISALRKETCNKSNMCESSKEALAEN 396
| | | | : : : : | | | | : : : : | | | | : : : : | | | | : : : :
Db 89 KLNLPKMEKDCGCGSGFNQAVCLIKTAGLLEQIYLDYLONEYEGNQENVRLQSSIR 148
: | | | | | | | | : | | : | | : | | : | | : | | : | | : | | :
QY 397 NLNLPKMAEKDGCQSGFQNETCLVKITGLLEFEVYLEYQNRFFESSEQARAVQMSTK 456
| | | | : : : : | | | | : : : : | | | | : : : : | | | | : : : :
Db 149 TLIQILKEKIAGL--ITTP--ATHTDLEKMOSSNEWKNKAKIILILRSLENFLQFLRA 204
||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : :
QY 457 VLIQFLQKAKNLDAITTPDTTNASLLTKLQAOQNLQDM-TTHILRSKFELQSSIRA 516
||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : :
Db 205 IR 206
QY 517 LR 518

RESULT 12
ENTRY ICMS6 #type complete
TITLE Interleukin-6 precursor - mouse
ALTERNATE_NAMES B-cell hybridoma growth factor; B-cell stimulating factor 2;
hepatocyte-stimulating factor; IL-6; interferon beta-II;
interleukin-HPI; myeloid differentiation inducer MGI-2A;
plasmacytoma growth factor
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change
22-Jun-1999
```

```

B-cell hybridomas.
#cross-references MUID:87092311
#accession A26662
##molecule_type protein
##residues 25-39,'X','41-42','X','44-45 ##label VSN
REFERENCE
A04086
#authors Chiu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.
#journal Proc. Natl. Acad. Sci. U.S.A. (1988) 85:7099-7103
#title Multiple biological activities are expressed by a mouse
interleukin 6 cDNA clone isolated from bone marrow stromal
cells.
#cross-references MUID:89017145
#accession A04086
##molecule_type mRNA
##residues 1-211 ##label CHI
##cross-references GB:J03783; NID:g198367; PIDN:AAA39301.1; PID:g309410
REFERENCE
A60799
#authors Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.
#journal Wolf, S.F.; Kamen, R.; Sachs, L.
Blood (1988) 72:2070-2073
#title The myeloid blood cell differentiation-inducing protein
MGI-2A is interleukin-6.
#cross-references MUID:89062753
#accession A60799
##molecule_type protein
##residues 77-98 ##label SHA
REFERENCE
SI0241
#authors Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
#journal J. Exp. Med. (1990) 171:965-970
#title DNA rearrangement and constitutive expression of the
interleukin 6 gene in a mouse plasmacytoma.
#cross-references MUID:90171860
#accession SI0241
##status preliminary
##molecule_type DNA
##residues 1-6 ##label BLA
##cross-references EMBL:X51457; NID:q49738; PIDN:CAA35824.1; PID:g58186
REFERENCE
S38254
#authors Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson,
R.J.
#journal Eur. J. Biochem. (1993) 217:53-59
#title Specific covalent modification of the tryptophan residues in
murine interleukin-6. Effect on biological activity and
conformational stability.
#cross-references MUID:94039075
#accession S38254
##status preliminary
##molecule_type protein
##residues 38-60;75,'X',77-79;176-203 ##label ZHA
GENETICS
#gene IL-6
#map_position 5
#introns 7/1; 68/3; 106/3; 156/3
CLASSIFICATION
#superfamily interleukin-6
KEYWORDS
Casleman's disease; cytokine; growth factor;
immunoregulation; lymphokine; macrophage; rheumatoid
arthritis
FEATURE
#domain signal sequence #status predicted #label SIG\
1-24 #product interleukin-6 #status experimental #label MAT
25-211 #length 211 #molecular-weight 24384 #checksum 5652
SUMMARY
Query Match 14.9%; Score 560; DB 1; Length 211;
Best Local Similarity 40.4%; Pred. No. 3.53e-84;
Matches 74; Conservative 50; Mismatches 56; Indels 3; Gaps 3;
Db 30 VRGDFTEF-TTPNR-EVYTTSQVGLTHVLVEMRKEKLCNGSDCMNDALAE NN 87
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 338 VPPGDSKDVAAAPHRQPLTSSERIDKQIRYILDGISA LRKETCTKSNMCKSEKALAE NN 397
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 88 LKPEIQRNDGCVQTGYNQEI CLKTSGLLEYSYLEYMKNNLKNKKDKARVLORDTE 147
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 398 LNLPKMAEKDGCQSFGNETCLVKITITGLFEVLYEQNR F-ESSERQARAVQMSTK 456
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```



```
#Journal      Genomics (1995) 25:157-163
#title        Genomic organization and chromosomal localization of the
               human and mouse genes encoding the alpha receptor component
               for ciliary neurotrophic factor.
#cross-references MUID:95293367
#accession     A56526
#molecule_type DNA
#residues      1-346,'S',348-372 #label VAL
#cross-references GB:L38025; NID:g608654; PIDN:AAA91337.1; PID:g608656
COMMENT        The CNTF receptor is attached to the membrane by a
glycosylphosphatidylinositol anchor.
COMMENT        The CNTF receptor sequence appears to contain several PEST regions.
GENETICS
#gene          GDB:CNTRF
#cross-references GDB:134652; OMIM:118946
#map_position 9p13-9p13
CLASSIFICATION #superfamily ciliary neurotrophic factor receptor; cytokine
               receptor homology; immunoglobulin homology
KEYWORDS       glycoprotein; growth factor receptor; membrane protein;
               phosphatidylinositol linkage
FEATURE
1-20           #domain signal sequence #status predicted #label SIG\
21-372         #product ciliary neurotrophic factor receptor #status
               predicted #label MAT\
39-91          #domain immunoglobulin homology #label IMM\
116-296        #domain cytokine receptor homology #label CRS\
46-89          #disulfide_bonds #status predicted\
60,70,142,190  #binding_site carbohydrate (Asn) (covalent) #status
               predicted
SUMMARY        #length 372 #molecular-weight 40649 #checksum 6224

Query Match      10.8%; Score 408; DB 1; Length 372;
Best Local Similarity 29.9%; Pred. No. 8 89e-54;
Matches 102; Conservative 86; Mismatches 129; Indels 24; Gaps 21;

Db 11 AVLAATAAVVYAAQHSPOAPHVQYERL-GSDVTLPC-GT-ANWDAAVTW--RVNGTDIA 65
QY 11 ALAAGAALAPRCAPQAEVARGVLTSLPGDSVTLTCTCGVEPEDNATVHWLKRKAAGSH 70

Db 66 PDLNG-SQ-LVLHGLHGLHGLYACFHRDWSHLRHQVLLHVGLPPREPVLSC-RSNTYP 122
QY 71 PSRWAGMGRLLRLSLVQLHDSGNSYCY-RAGRPAGTVHLL-VDPVPEEPQLSCFRKSPLS 128

Db 123 KGFYCSW-HLPTPTYPNT-FNVTVLHGS--KIMV-CE-KDPALKNRCHIRYMHLESTI 175
QY 129 NVV-CEWGRSTPSTLTAKVLLYRKFNQSPAEQFQPCOYSQESQKFSQCLAVPEGDSF 187

Db 176 KYKVSISVSNALGHN-ATAITDEFITVKPDPPENNVARVPSPNRRLEVLTWQTPSTWPD 234
QY 188 -YIVSMCVASSVGSFKSTQTFQCGGILQPDPPANITVTAVARNPRLSVTWQDPHSW-N 245

Db 235 PESFPLKFTLYRPLLDQWQHVELSDGTAH-TTIDAYAGKEYIIQVAAKDN-EIGTWSD 292
QY 246 SSFYRLRFELRYRAERSKSTFTTMMVKDLQHHCVIHDAMSGLRHVYVQLRAQEEFGGE 305

Db 293 WSAVAHAATPTEPRHLTTEAOAAETTTSTSSLAPPTTK 333
QY 306 WSPFAMGTPWTE-SRSPFARGGGGGGGGVPEPPGEDSK 345
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Search completed: Thu Aug 10 16:15:17 2000
Job time : 95 secs.

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W P S R L H (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Aug 10 16:19:36 2000; MasPar time 10.55 Seconds
Tabular output not generated. 711.501 Million cell updates/sec

Title: >US-09-142-471-4
Description: (1-520) from US09142471.pep
Perfect Score: 3771
Sequence: 1 MLAVGALLAALLAAPGAAL.....LILRSKFLOSSLRALRQM 520

Scoring table: PAM 150
Gap 11

Searched: 145341 seqs, 14437480 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Statistics: Mean 34.924; Variance 189.856; scale 0.184

Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2398	63.6	344	5	5480796-7 atent No. 5480796	3.44e-175
2	2398	63.6	344	5	5171840-7 atent No. 5171840	3.44e-175
3	2398	63.6	468	5	5480796-2 atent No. 5480796	3.44e-175
4	2398	63.6	468	5	5171840-2 atent No. 5171840	3.44e-175
5	2394	63.5	323	5	5480796-6 atent No. 5480796	7.12e-175
6	2394	63.5	323	5	5171840-6 atent No. 5171840	7.12e-175
7	1542	40.9	386	5	5480796-5 atent No. 5480796	7.67e-108
8	1542	40.9	386	5	5171840-5 atent No. 5171840	7.67e-108
9	1337	35.5	317	4	PCT-US95-0 Sequence 145, Applicat	8.45e-92
10	1337	35.5	317	3	US-08-469- Sequence 145, Applicat	8.45e-92
11	1306	34.6	201	5	5171840-11 atent No. 5171840	2.23e-89
12	1289	34.2	186	4	PCT-US94-1 Sequence 20, Applicati	4.74e-88
13	1289	34.2	186	3	US-08-469- Sequence 163, Applicat	4.74e-88
14	1289	34.2	186	1	US-08-165- Sequence 20, Applicati	4.74e-88
15	1289	34.2	186	4	PCT-US95-0 Sequence 163, Applicati	4.74e-88
16	1289	34.2	186	1	US-07-632- Sequence 20, Applicati	4.74e-88
17	1289	34.2	186	1	US-07-745- Sequence 20, Applicati	4.74e-88
18	1289	34.2	186	1	US-07-745- Sequence 20, Applicati	4.74e-88
19	1287	34.1	184	2	US-08-567- Sequence 2, Applicatio	6.79e-88
20	1287	34.1	184	1	US-08-567- Sequence 2, Applicatio	6.79e-88
21	1287	34.1	184	5	5186931-1 atent No. 5186931	6.79e-88
22	1287	34.1	185	1	US-07-918- Sequence 2, Applicatio	6.79e-88
23	1287	34.1	185	1	US-08-246- Sequence 5, Applicatio	6.79e-88

24	1287	34.1	185	1	US-08-231- Sequence 2, Applicatio	6.79e-88
25	1287	34.1	185	2	US-08-766- Sequence 5, Applicatio	6.79e-88
26	1287	34.1	185	1	US-07-632- Sequence 1, Applicatio	6.79e-88
27	1287	34.1	185	2	US-08-716- Sequence 7, Applicatio	6.79e-88
28	1287	34.1	185	5	5186931-2 atent No. 5186931	6.79e-88
29	1287	34.1	185	4	PCT-US93-0 Sequence 2, Applicatio	6.79e-88
30	1287	34.1	187	1	US-07-632- Sequence 3, Applicatio	6.79e-88
31	1287	34.1	212	1	US-08-792- Sequence 9, Applicatio	6.79e-88
32	1287	34.1	212	5	5510472-2 atent No. 5510472	6.79e-88
33	1283	34.0	185	1	US-08-231- Sequence 6, Applicatio	1.39e-87
34	1283	34.0	185	1	US-07-918- Sequence 6, Applicatio	1.39e-87
35	1283	34.0	185	4	PCT-US93-0 Sequence 1, Applicatio	1.39e-87
36	1279	33.9	183	1	US-08-009- Sequence 2, Applicatio	2.86e-87
37	1280	33.9	184	2	US-08-693- Sequence 2, Applicatio	2.39e-87
38	1280	33.9	184	2	US-09-008- Sequence 4, Applicatio	4.10e-87
39	1277	33.9	185	1	US-08-231- Sequence 4, Applicatio	4.10e-87
40	1277	33.9	185	1	US-07-918- Sequence 4, Applicatio	4.10e-87
41	1277	33.9	185	4	PCT-US93-0 Sequence 8, Applicatio	4.10e-87
42	1273	33.8	185	4	PCT-US93-0 Sequence 8, Applicatio	4.10e-87
43	1273	33.8	185	1	US-08-231- Sequence 8, Applicatio	8.41e-87
44	1273	33.8	185	1	US-07-918- Sequence 8, Applicatio	8.41e-87
45	1261	33.4	186	1	US-08-209- Sequence 2, Applicatio	7.27e-86

ALIGNMENTS

RESULT 1
ID 5480796-7 STANDARD; PRT; 344 AA.
XX
AC xxxxxx
XX
DF
DT
DE
DE Patent No. 5480796
XX
XX Patent No. 5480796
CC APPLICANT: KISHIMOTO, TADAMITSU
CC TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
CC FOR HUMAN B CELL STIMULATORY FACTOR-2
CC NUMBER OF SEQUENCES: 8
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/907,650
CC FILING DATE: 02-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 298,694
CC FILING DATE: 19-JAN-1989
CC SEQ ID NO:7
CC LENGTH: 344
CC SEQUENCE 344 AA; 38047 MW; 637889 CN;

Query Match 63.6%; Score 2398; DB 5; Length 344;
Best Local Similarity 100.0%; Pred. No. 3.44e-175;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLAVGALLAALLAAPGAALAPRCAPQAEVARGVLTSLPGSDSVTLTCGPEPEDNATVHW 60
|||||
Qy 1 MLAVGALLAALLAAPGAALAPRCAPQAEVARGVLTSLPGSDSVTLTCGPEPEDNATVHW 60
|||||

Db 61 VLURKPAAGSHPSRWAGMGRLLRLSRVQLHDSGNYSCYRAGRAGTAVHLLVDVPPPEPQLS 120
Qy 61 VLURKPAAGSHPSRWAGMGRLLRLSRVQLHDSGNYSCYRAGRAGTAVHLLVDVPPPEPQLS 120
|||||

Db 121 CPERKPLSNVNCWEWGRPSLTTKAVLLVRKFQNSPAEDFOEPCOYSOESOKFSCOLAV 180
Qy 121 CPERKPLSNVNCWEWGRPSLTTKAVLLVRKFQNSPAEDFOEPCOYSOESOKFSCOLAV 180
|||||

Db 181 PGEDSSFYIVSMCVASSVSGSKFSKTQTFCGCGILOPDPANITVTAVARNRWLSVTWQD 240
Qy 181 PGEDSSFYIVSMCVASSVSGSKFSKTQTFCGCGILOPDPANITVTAVARNRWLSVTWQD 240
|||||

Db 241 PHSWNSSFYRLRFELRYRAERSKTFWTMMVKDLQHHCVITHDAWSGLRHVVQLRAQEEFGQ 300
Qy 241 PHSWNSSFYRLRFELRYRAERSKTFWTMMVKDLQHHCVITHDAWSGLRHVVQLRAQEEFGQ 300
|||||

DE	Patent No.	5171840
XX		
CC	Patent No.	5171840
CC	APPLICANT:	KISHIMOTO, TADAMITSU
CC	TITLE OF INVENTION:	RECEPTOR PROTEIN FOR HUMAN B CELL
CC	STIMULATORY FACTOR-2	
CC	NUMBER OF SEQUENCES:	11
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	US/07/298,694
CC	FILING DATE:	19-JAN-1989
CC	SEQ ID NO:6:	
CC	LENGTH:	323
SQ	SEQUENCE	323 AA; 35744 MW; 577074 CN;
	Query Match	63.5%; Score 2394; DB 5; Length 323;
	Best Local Similarity	100.0%; Pred. No. 7.12e-175;
	Matches	322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dd	1	MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVPEPDNATVHW 60
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Dd	61	VLRKPAAGSHPSRWAGMRLLILRSVLQHDSGNYS CYRAGRPA GTVHLLVDVPPEEPQLS 120
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Dd	121	CFRKSPLSNNVCWGPRTSPSLTTKAVLLVRKFQNSPAEDFQPCQYSQSOKFSCOLAV 180
QY	121	CFRKSPLSNNVCWGPRTSPSLTTKAVLLVRKFQNSPAEDFQPCQYSQSOKFSCOLAV 180
Dd	181	PEGDSSFYIIVSMCVASSVGSKFTQTFCGIGILQDPDPANIITVAVARNPRLSVTWQD 240
QY	181	PEGDSSFYIIVSMCVASSVGSKFTQTFCGIGILQDPDPANIITVAVARNPRLSVTWQD 240
Dd	241	PHSWNSSFYELRELRYRAERSKTFTTMVKDLQHCVIHDANSGLRHVVQLRAQEFGQ 300
QY	241	PHSWNSSFYELRELRYRAERSKTFTTMVKDLQHCVIHDANSGLRHVVQLRAQEFGQ 300
Dd	301	GEMSEWSPEAMGTPWTESRPP 322
QY	301	GEMSEWSPEAMGTPWTESRPP 322
RESULT	7	
ID	5480796-5	STANDARD; PRT; 386 AA.
XX	AC	xxxxxx
XX	DT	
XX	DE	
XX	DE	Patent No. 5480796
CC	Patent No.	5480796
CC	APPLICANT:	KISHIMOTO, TADAMITSU
CC	TITLE OF INVENTION:	ANTIBODIES AGAINST THE RECEPTOR PROTEIN
CC	FOR HUMAN B CELL STIMULATORY FACTOR-2	
CC	NUMBER OF SEQUENCES:	8
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	US/07/907,650
CC	FILING DATE:	02-JUL-1992
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	298,694
CC	FILING DATE:	19-JAN-1989
CC	SEQ ID NO:5:	
CC	LENGTH:	386
SQ	SEQUENCE	386 AA; 42734 MW; 827023 CN;
	Query Match	40.9%; Score 1542; DB 5; Length 386;
	Best Local Similarity	98.1%; Pred. No. 7.67e-108;
	Matches	212; Conservative 0; Mismatches 0; Indels 4; Gaps 2;
Dd	28	VDVPPEEPQLSCFRKSPLSNVVC--GPRSTPEWSLTTKAVLLVRKFQNSPAEDFQPCQY 85

CC	MEDIUM TYPE:	317 AA; 35632 MW; 490978 CN;	
CC	COMPUTER:	IBM PC compatible	
CC	OPERATING SYSTEM:	PC-DOS/MS-DOS	
CC	SOFTWARE:	PatentIn Release #1.0, Version #1.30 (EPO)	
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER:	PCJ/US95/01185	
CC	FILING DATE:	02-FEB-1995	
CC	CLASSIFICATION:		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER:	US 08/192325	
CC	FILING DATE:	14-FEB-1994	
CC	INFORMATION FOR SEQ ID NO:	145:	
CC	SEQUENCE CHARACTERISTICS:		
CC	LENGTH:	317 amino acids	
CC	TYPE:	amino acid	
CC	STRANDEDNESS:		
CC	TOPOLOGY:	linear	
CC	MOLECULE TYPE:	protein	
CC	SEQUENCE	317 AA; 35632 MW; 490978 CN;	
CC	Query Match	35.5%; Score 1337; DB 4; Length 317;	
CC	Best Local Similarity	97.9%; Pred. NO. 8.45e-92;	
CC	Matches	191; Conservative 3; Mismatches 1; Indels 0;	
Db	123	GGGGGGGNSMVPVPPGDSKDVAAPHRPQLTSSERIDKQIRYILDGTSALRKETCNKS	
Qy	326	GGGGGGGSGVPPVPPGDSKDVAAPHRPQLTSSERIDKQIRYILDGTSALRKETCNKS	
Db	183	CESSEKALAEANNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLEYLQNRRES	
Qy	386	CESSEKALAEANNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLEYLQNRRES	
Db	243	EQARAVOMSTKVLQIFQKKAKNLDAITTPDPTTNASLLTKLQAOQWLODMTHLLIL	
Qy	446	EQARAVOMSTKVLQIFQKKAKNLDAITTPDPTTNASLLTKLQAOQWLODMTHLLIL	
Db	303	KFEFLQSSLRALQM 317	
Qy	506	KFEFLQSSLRALQM 520	
RESULT	10		
ID	US-08-469-318-145	STANDARD;	PRT; 317 AA.
XX	xxxxxx		
XX			
XX			
DT			
XX			
XX			
DE			
XX			
CC	Sequence 145, Application US/08469318		
CC	Sequence 145, Application US/08469318		
CC	Patent No. 6022535		
CC	GENERAL INFORMATION:		
CC	APPLICANT:		
CC	TITLE OF INVENTION:	Multivariant IL-3 Hematopoiesis Fusion	
CC	TITLE OF INVENTION:	Protein	
CC	NUMBER OF SEQUENCES:	196	
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE:	Floppy disk	
CC	COMPUTER:	IBM PC compatible	
CC	OPERATING SYSTEM:	PC-DOS/MS-DOS	
CC	SOFTWARE:	PatentIn Release #1.0, Version #1.30 (EPO)	
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER:	US/08/469,318	
CC	FILING DATE:		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER:	08/446,872	
CC	FILING DATE:		
CC	INFORMATION FOR SEQ ID NO:	145:	
CC	SEQUENCE CHARACTERISTICS:		
CC	LENGTH:	317 amino acids	
CC	TYPE:	amino acid	

DE Sequence 163, Application US/08469318
XX
CC Sequence 163, Application US/08469318
CC Patent No. 6022535
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
CC TITLE OF INVENTION: Protein
CC NUMBER OF SEQUENCES: 196
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/469,318
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/446,872
CC FILING DATE:
CC INFORMATION FOR SEQ ID NO: 163:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 186 amino acids
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 186 AA; 21112 MW; 171066 CN;

Query Match 34.2%; Score 1289; DB 3; Length 186;
Best Local Similarity 98.9%; Pred. No. 4.74e-88;
Matches 184; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MAPVPPGDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKNMCESSKEALA 60
QY 335 VEPVPPGDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKNMCESSKEALA 394

Db 61 ENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVILEYLNRFESSEEQARAVQMS 120
QY 395 ENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVILEYLNRFESSEEQARAVQMS 454

Db 121 TKVLIQFLQKAKNLDAITTPDPTNASLTKLQAOQNQLDMTTHILRSFKFQSSL 180
QY 455 TKVLIQFLQKAKNLDAITTPDPTNASLTKLQAOQNQLDMTTHILRSFKFQSSL 514

Db 181 RALRQM 186
QY 515 RALRQM 520

RESULT 14
ID US-08-165-301A-20 STANDARD; PRT; 186 AA.

XX AC xxxxxx

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Sequence 20, Application US/08165301A

Sequence 20, Application US/08165301A

Patent No. 5646016

GENERAL INFORMATION:

APPLICANT: McCoy, John

APPLICANT: DiBlasio-Smith, Elizabeth

APPLICANT: Grant, Kathleen

APPLICANT: Lavallie, Edward R.

TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO

TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES, AND MODIFIED

TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

CC STREET: 87 CambridgePark Drive
CC CITY: Cambridge
CC STATE: Massachusetts
CC COUNTRY: U.S.A.
CC ZIP: 02140
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/165,301A
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Meiner, M. C.
CC REGISTRATION NUMBER: 33,544
CC REFERENCE/DOCKET NUMBER: GI 5188D
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (617) 876-1170
CC TELEFAX: (617) 876-5851
CC INFORMATION FOR SEQ ID NO: 20:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 186 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 186 AA; 21112 MW; 171066 CN;

Query Match 34.2%; Score 1289; DB 1; Length 186;

Best Local Similarity 98.9%; Pred. No. 4.74e-88;

Matches 184; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MAPVPPGDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKNMCESSKEALA 60

QY 335 VEPVPPGDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKNMCESSKEALA 394

Db 61 ENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVILEYLNRFESSEEQARAVQMS 120

QY 395 ENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVILEYLNRFESSEEQARAVQMS 454

Db 121 TKVLIQFLQKAKNLDAITTPDPTNASLTKLQAOQNQLDMTTHILRSFKFQSSL 180

QY 455 TKVLIQFLQKAKNLDAITTPDPTNASLTKLQAOQNQLDMTTHILRSFKFQSSL 514

Db 181 RALRQM 186

QY 515 RALRQM 520

RESULT 15
ID US-07-921-848-20 STANDARD; PRT; 186 AA.

XX AC xxxxxx

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XX CC

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XX CC

XX CC

XX CC

Sequence 20, Application US/07921848

Sequence 20, Application US/07921848

Patent No. 5292646

GENERAL INFORMATION:

APPLICANT: McCoy, John

APPLICANT: Lavallie, Edward

TITLE OF INVENTION: Peptide and Protein Fusions To

TITLE OF INVENTION: Thioresoxin and Thioresoxin-Like Molecules

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

```

CC      ZIP: 02140
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/07/921,848
CC      FILING DATE: 19920728
CC      CLASSIFICATION: 435
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 07/652,531
CC      FILING DATE: 06-FEB-1991
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 07/745,382
CC      FILING DATE: 14-AUG-1991
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Cseir, Luann
CC      REGISTRATION NUMBER: 31,822
CC      REFERENCE/DOCKET NUMBER: G15188A
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (617) 876-1170
CC      TELEFAX: (617) 876-5851
CC      INFORMATION FOR SEQ ID NO: 20:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 186 amino acids
CC      TYPE: AMINO ACID
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 186 AA; 21112 MW; 171066 CN;

Query Match      34.2%; Score 1289; DB 1; Length 186;
Best Local Similarity 98.9%; Pred. No. 4,74e-88;
Matches 184; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MAPVPPGDSKDVAAAPHRQPLTSSERIDKOIRYILDGIALRKETCNKNCMCSSKEALA 60
QY : |||||
335 VEPVPPGDSKDVAAAPHRQPLTSSERIDKOIRYILDGIALRKETCNKNCMCSSKEALA 394
Db 61 ENNLNLPKMAEKDGCFCQSGFNEETCLVKIITGLLEFEVYLEYLQNFESSEEQARAVQMS 120
QY : |||||
395 ENNLNLPKMAEKDGCFCQSGFNEETCLVKIITGLLEFEVYLEYLQNFESSEEQARAVQMS 454
Db 121 TKVLIQFLQKKAKNLDAITTPDPTTNASLITKIQANQWLQDMTTHLILRSFKFLOSSL 180
QY : |||||
455 TKVLIQFLQKKAKNLDAITTPDPTTNASLITKIQANQWLQDMTTHLILRSFKFLOSSL 514
Db 181 RALRQM 186
QY : |||||
515 RALRQM 520

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Search completed: Thu Aug 10 16:20:27 2000
Job time : 51 secs.

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W P S R L
***** (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Aug 10 16:12:21 2000; MasPar time 16.72 Seconds
Tabular output not generated. 736.510 Million cell updates/sec

Title: >US-09-142-471-4
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Perfect Score: 3771
Sequence: 1 MLAVGCALLAALLAAPGAAL.....LILRSKFQSSLRALRQM 520
Scoring table: PAM 150
Gap 11
Searched: 188963 seqs, 23686106 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a-geneseq36
1:geneseqp
Statistics: Mean 37.159; Variance 190.226; scale 0.195

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
Result No.	Score	Query %	Match	Length	DB ID	Description	Pred. No.		
1	3716	98.5	525	1	W36846	Human fusion polypepti	7.34e-296		
2	3458	91.7	543	1	W03164	Chimeric sIL-6R/IL-6 p	3.62e-274		
3	3390	89.9	500	1	W36847	Human fusion polypepti	1.88e-268		
4	2398	63.6	344	1	P90528	B cell stimulating fac	3.10e-185		
5	2398	63.6	468	1	R37215	IL-6 receptor.	3.10e-185		
6	2398	63.6	468	1	P30284	Sequence of a receptor	1.19e-184		
7	2391	63.4	360	1	W70804	Amino acid sequence of	9.84e-185		
8	2392	63.4	468	1	R98364	Interleukin-6 receptor	1.45e-184		
9	2390	63.4	468	1	P90525	B cell stimulating fac	3.10e-185		
10	2391	63.4	592	1	W70797	Human interleukin-6R-a	1.19e-184		
11	2373	62.9	468	1	W71371	Human interleukin-6 re	3.83e-183		
12	2351	62.3	323	1	P90527	B cell stimulating fac	2.66e-181		
13	2317	61.4	315	1	W70805	Amino acid sequence of	1.86e-178		
14	2110	56.0	1042	1	R70122	IL8-R type 1-GPB 130 f	3.77e-161		
15	1534	40.7	386	1	P90526	B cell stimulating fac	3.78e-113		
16	1368	36.3	182	1	W00403	Interleukin-6 antagoni	2.24e-99		
17	1320	35.0	460	1	R13318	IL-6R for soluble IL-6	2.12e-95		
18	1311	34.8	460	1	R13318	IL-6 receptor.	1.18e-94		
19	1289	34.2	186	1	P80270	Recombinant interleuki	7.79e-93		
20	1289	34.2	186	1	R75765	Human interleukin-6.	7.79e-93		
21	1287	34.1	184	1	R03914	Polypeptide with human	1.14e-92		
22	1287	34.1	184	1	R52526	Interleukin 6.	1.14e-92		
23	1287	34.1	184	1	P81158	Polypeptide with B-cel	1.14e-92		

24	1287	34.1	184	1	R20783	Interleukin-6.	1.14e-92		
25	1287	34.1	184	1	R54990	Mutant Interleukin 6 S	1.14e-92		
26	1287	34.1	184	1	W02609	Interleukin-6.	1.14e-92		
27	1287	34.1	184	1	R06532	Human B-cell simulator	1.14e-92		
28	1287	34.1	184	1	R86623	B-cell differentiation	1.14e-92		
29	1287	34.1	185	1	R05274	Segment of human B cel	1.14e-92		
30	1287	34.1	185	1	W00130	Human interleukin-6 fr	1.14e-92		
31	1287	34.1	185	1	R05275	Segment of human B cel	1.14e-92		
32	1287	34.1	185	1	R68624	Ala-BCDF.	1.14e-92		
33	1287	34.1	187	1	R13471	hIL-6 protein.	1.14e-92		
34	1287	34.1	188	1	W35011	Human interleukin-6 (I	1.14e-92		
35	1287	34.1	208	1	R81160	Polypeptide with B-cel	1.14e-92		
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41	1287	34.1	212	1	R49249	Sequence of human B-ce	1.14e-92		
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45	1287	34.1	212	1	P90436	Interferon-beta-2.	1.14e-92		

ALIGNMENTS

RESULT 1
ID W36846 standard; Protein; 525 AA.
AC W36846; (first entry)
DT 23-MAR-1998
DE Human fusion polypeptide H-IL-6 with 18 amino acid linker.
KW Interleukin-6; IL-6; Interleukin-6 receptor; IL-6R; ligand; conjugate;
KW protein interaction; therapeutic; antagonist.
OS Synthetic.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= signal_peptide
FT Protein 20..524
FT /note= "H-IL-6 fusion polypeptide"
FT Region 324..341
FT /label= linker region
FT FT /note= "Links together COOH-terminus of sIL-6R with the NH2-terminus of IL-6"
PN W09732891-A2.
PD 12-SEP-1997.
PF 07-MAR-1997; D00458.
PR 07-MAR-1996; DE-008813.
PA (ANGE-) ANGEWANDTE GENTECHNOLOGIE SYSTEME GMBH.
PI Rose-John S;
PI WPI: 97-470536/43.
DR N-PSDB; T97848.
DR Conjugate of two peptide(s) with mutual affinity connected by a
PT linker - used to modulate interactions between proteins, e.g. for ex
PT vivo expansion of human stem cells
PS Disclosure; Fig 1; 19pp; German.
CC This sequence represents the fusion polypeptide H-IL-6 which contains
CC an 18 amino acid linker which joins the carboxy terminus of human
CC interleukin-6 receptor (IL-6R) with the amino terminus of human
CC interleukin-6 (IL-6). Such conjugates could be used to modulate
CC interactions between proteins, particularly to overcome interrupted
CC interactions caused by an incomplete interleukin-6 (IL-6) receptor. These
CC constructs derived from IL-6 and its receptor, can also be used for ex
CC vivo expansion of human stem cells, and as a therapeutic IL-6 receptor
CC antagonist.
SQ Sequence 525 AA;
Query Match 98.5%; Score 3716; DB 1: Length 525;
Best Local Similarity 99.0%; Pred. No. 7.34e-296;
Matches 520; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
Db 1 MLAVGCALLAALLAAPGAALPRRCPAQEVARGVLTSLPGDSVTLTCPCVPEPDNATVHW 60
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QY 1 MLAVGCALLAALAAAPCAALAPRRCPAQEVARGLTSLPGDSVTLTCTCPGVEPNATVHW 60
 Db 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSYRAGRPAAGTGHLLVDVPPPEPQLS 120
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 Db 121 CFRKSPLSNVVCEWGPSTPSLTAKVLLVRKFNQSPAEDEFQPCQYQSQSKFSCQLAV 180
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 Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVAVARNPRLSVTWQD 240
 QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVAVARNPRLSVTWQD 240
 Db 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCIVHDAMSLRHVVQLRAQEEFG 300
 QY 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCIVHDAMSLRHVVQLRAQEEFG 300
 Db 301 GEWSESPAMGTPWTESRPPARGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 360
 QY 301 GEWSESPAMGTPWTESRPPARGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 360
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 Db 481 DPTTNASLLTKLQANQWLDMTTHLLRSFKFLOSSLRALROM 525
 QY 476 DPTTNASLLTKLQANQWLDMTTHLLRSFKFLOSSLRALROM 520

RESULT 2
 ID Y03164 standard; protein; 543 AA.
 AC Y03164;
 DT 11-JUN-1999 (first entry)
 DE Chimeric sIL-6/IL-6 protein.
 KW Soluble interleukin-6 receptor; interleukin-6; sIL-6; IL-6; sIL-6/IL-6;
 KW chimeric protein; fusion protein; cell growth inhibitor; melanoma cell;
 KW highly malignant cancer cell; in vivo engraftment; mammalian cancer;
 KW human haematopoietic cell; bone marrow transplantation; mammalian cancer;
 KW hepatotoxic agent protection; haematopoiesis; liver disorder;
 KW neurological disorder.
 OS Synthetic.
 PN WO902552-A2.
 PS Claim 6; Fig 3; 77pp; English.
 PD 21-JAN-1999.
 PF 09-JUL-1998; IL0321.
 PR 30-DEC-1997; IL-122818.
 PR 10-JUL-1997; IL-121284.
 PA (VEDA) YEDA RES & DEV CO LTD.
 PI Chebeth J, Kollet O, Lapidot T, Revel M;
 DR WPI: 99-120776/10
 PT New glycosylated soluble IL-6 receptor/IL-6 conjugates - used for
 PT e.g. treating cancers, bone marrow transplantation, increasing
 PT haematopoiesis or treating liver or neurological disorders
 PS Claim 6; Fig 3; 77pp; English.
 CC This sequence represents the chimeric glycosylated soluble interleukin-6
 CC receptor (sIL-6R)-interleukin-6 (IL-6) protein (sIL-6R/IL-6) of the
 CC invention. It comprises a fusion protein product between all of the
 CC naturally occurring form of sIL-6R and all of the naturally occurring
 CC form of IL-6, the sIL-6/IL-6 and analogues being glycosylated in a
 CC similar fashion to the glycosylation of naturally occurring sIL-6R and
 CC IL-6. The sIL-6R/IL-6 and analogues are capable of inhibiting the
 CC growth of highly malignant cancer cells, e.g. melanoma cells, eliciting
 CC the in vivo engraftment of human haematopoietic cells in bone marrow
 CC transplantation and protecting liver from hepatotoxic agents.
 CC They can be used for the preparation of a medicament for treating
 CC mammalian cancers by way of inhibition of cancer cells, for enhancement
 CC of bone marrow transplantation by way of eliciting engraftment of human
 CC haematopoietic cells in bone marrow transplantation, for increasing

CC haematopoiesis, for treating liver or neurological disorders, or in other
 CC applications in which IL-6 or sIL-6R are used.
 SQ Sequence 543 AA;

Query Match 91.7%; Score 3458; DB 1; Length 543;
 Best Local Similarity 94.1%; Pred. No. 3.62e-274;
 Matches 511; Conservative 3; Mismatches 6; Indels 23; Gaps 4;

Db 1 MLAVGCALLAALAAAPCAALAPRRCPAQEVARGLTSLPGDSVTLTCTCPGVEPNATVHW 60
 QY 1 MLAVGCALLAALAAAPCAALAPRRCPAQEVARGLTSLPGDSVTLTCTCPGVEPNATVHW 60
 Db 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSYRAGRPAAGTGHLLVDVPPPEPQLS 120
 QY 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSYRAGRPAAGTGHLLVDVPPPEPQLS 120
 Db 121 CFRKSPLSNVVCEWGPSTPSLTAKVLLVRKFNQSPAEDEFQPCQYQSQSKFSCQLAV 180
 QY 121 CFRKSPLSNVVCEWGPSTPSLTAKVLLVRKFNQSPAEDEFQPCQYQSQSKFSCQLAV 180
 Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVAVARNPRLSVTWQD 240
 QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVAVARNPRLSVTWQD 240
 Db 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCIVHDAMSLRHVVQLRAQEEFG 300
 QY 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCIVHDAMSLRHVVQLRAQEEFG 300
 Db 301 GEWSESPAMGTPWTESRPPARGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 360
 QY 301 GEWSESPAMGTPWTESRPPARGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 360
 Db 361 VPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGIALRKETCNKSNMCESSKEALAEEN 420
 QY 361 VPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGIALRKETCNKSNMCESSKEALAEEN 420
 Db 421 LNLPKMAEKDCGFCGFSQGFNEETCLVKIITGLLEFEVYLYLQNRFSSEEQARAVOMSTKV 480
 QY 421 LNLPKMAEKDCGFCGFSQGFNEETCLVKIITGLLEFEVYLYLQNRFSSEEQARAVOMSTKV 480
 Db 481 LIQFLQKAKNLDALTTPDPTTNASLLTKLQANQWLDMTTHLLRSFKFLOSSLRAL 540
 QY 481 LIQFLQKAKNLDALTTPDPTTNASLLTKLQANQWLDMTTHLLRSFKFLOSSLRAL 540
 Db 541 ROM 543
 QY 518 ROM 520

RESULT 3
 ID W36847 standard; Protein; 500 AA.
 AC W36847;
 DT 25-MAR-1998 (first entry)
 DE Human fusion polypeptide H-IL-6 with 13 amino acid linker.
 KW Interleukin-6; IL-6; interleukin-6 receptor; IL-6R; ligand; conjugate;
 KW protein interaction; therapeutic; antagonist.
 OS Synthetic.
 OS Homo sapiens.
 FH Key
 FT Peptide
 FT Protein
 FT Region
 FT Location/Qualifiers
 1. .19
 /label= signal_peptide
 20. .500
 /note= "H-IL-6 fusion polypeptide"
 304. .316
 /label= linker region
 /note= "Links together COOH-terminus of sIL-6R with
 the NH2-terminus of IL-6"
 WO9732891-A2.
 PD 12-SEP-1997.
 PF 07-MAR-1997; D00458.
 PR 07-MAR-1996; DE-008813.
 PA (ANGE-) ANGEWANDTE GENTECHNOLOGIE SYSTEME GMBH.
 PI Rose-John S;

DR WPI; 97-470536/43.
 DR N-PSDB; T97849.
 PT Conjugate of two peptide(s) with mutual affinity connected by a
 PT linker - used to modulate interactions between proteins, e.g. for ex
 PT vivo expansion of human stem cells
 PS Disclosure; Fig 2; 19pp; German.
 CC This sequence represents the fusion polypeptide H-IL-6 which contains
 CC an 13 amino acid linker which joins the carboxy terminus of human
 CC interleukin-6 receptor (IL-6R) with the amino terminus of human
 CC interleukin-6 (IL-6). Such conjugates could be used to modulate
 CC interactions between proteins, particularly to overcome interrupted
 CC interactions caused by an incomplete interleukin-6 (IL-6) receptor. These
 CC constructs derived from IL-6 and its receptor, can also be used for ex
 CC vivo expansion of human stem cells, and as a therapeutic IL-6 receptor
 CC antagonist.
 SQ Sequence 500 AA;

Query Match 89.9%; Score 3390; DB 1; Length 500;
 Best Local Similarity 96.2%; Pred. No. 1.88e-268;
 Matches 500; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

Db 1 MLAVGCCALLAALAPGAALAPRCAPAEVARGVLTSLPGDSVTLTCTGVEPEDNATVHW 60
 QY 1 MLAVGCCALLAALAPGAALAPRCAPAEVARGVLTSLPGDSVTLTCTGVEPEDNATVHW 60
 Db 61 VLKPPAAGSHPSRWAGMRLLRSVQLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
 QY 61 VLKPPAAGSHPSRWAGMRLLRSVQLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
 Db 121 CFRKSPLSNVVCEWGPSTSLTAKVLLVRKFNQSPAEFQEPQYQSQKFSQCLAV 180
 QY 121 CFRKSPLSNVVCEWGPSTSLTAKVLLVRKFNQSPAEFQEPQYQSQKFSQCLAV 180
 Db 181 PEGDSSFYIYVMCVASSVSGSKFTQFGCGIILQPPPPANITVAVARNPRLSVTWQD 240
 QY 181 PEGDSSFYIYVMCVASSVSGSKFTQFGCGIILQPPPPANITVAVARNPRLSVTWQD 240
 Db 241 PHSNWSFYRLRFLRYRAERSKFTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEEFG 300
 QY 241 PHSNWSFYRLRFLRYRAERSKFTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEEFG 300
 Db 301 GEWSESPAMGTPWTSRSPPA 323
 QY 301 GEWSESPAMGTPWTSRSPPA 323

RESULT 4
 ID P90528 standard; protein; 344 AA.
 AC P90528;
 DT 25-JAN-1990 (first entry)
 DE B cell stimulating factor-2 receptor.
 KW B cell stimulating factor-2 receptor; monocytic U937 cell line.
 OS Homo sapiens.
 PN A08928720-A.
 PF 27-JUL-1989.
 PR 23-JAN-1989; 028720.
 PR 22-JAN-1988; JP-012387.
 PR 25-JAN-1988; JP-012599.
 PR 04-AUG-1988; JP-194885.
 PR 14-JAN-1989; JP-007461.
 PA (KISH) Tadimitsu Kishimoto.

PI Kishimoto T;
 DR WPI; 89-264012/37.
 DR N-PSDB; P90525.
 PT Receptor protein for human B cell stimulating factor-2 - used for
 PT developing prophylactic, therapeutic and diagnostic agents for
 PT associated disorders.
 PS Claim 7; page 40; 76pp; English.
 CC The BSF2 receptor has amino acids at the C-terminal deleted. The receptor
 CC is derived from a monocytic U937 cell line. It can be used to develop
 CC prophylactic and therapeutic pharmaceuticals, as agents to relate
 CC diseases and disorders to abnormal BSF-2 prodn. It can also be used to
 CC study an immune mechanism with which BSF-2 or the receptor is concerned.
 SQ Sequence 344 AA;

Query Match 63.6%; Score 2398; DB 1; Length 344;
 Best Local Similarity 100.0%; Pred. No. 3.10e-185;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLAVGCCALLAALAPGAALAPRCAPAEVARGVLTSLPGDSVTLTCTGVEPEDNATVHW 60
 QY 1 MLAVGCCALLAALAPGAALAPRCAPAEVARGVLTSLPGDSVTLTCTGVEPEDNATVHW 60
 Db 61 VLKPPAAGSHPSRWAGMRLLRSVQLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
 QY 61 VLKPPAAGSHPSRWAGMRLLRSVQLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
 Db 121 CFRKSPLSNVVCEWGPSTSLTAKVLLVRKFNQSPAEFQEPQYQSQKFSQCLAV 180
 QY 121 CFRKSPLSNVVCEWGPSTSLTAKVLLVRKFNQSPAEFQEPQYQSQKFSQCLAV 180
 Db 181 PEGDSSFYIYVMCVASSVSGSKFTQFGCGIILQPPPPANITVAVARNPRLSVTWQD 240
 QY 181 PEGDSSFYIYVMCVASSVSGSKFTQFGCGIILQPPPPANITVAVARNPRLSVTWQD 240
 Db 241 PHSNWSFYRLRFLRYRAERSKFTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEEFG 300
 QY 241 PHSNWSFYRLRFLRYRAERSKFTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEEFG 300
 Db 301 GEWSESPAMGTPWTSRSPPA 323
 QY 301 GEWSESPAMGTPWTSRSPPA 323

RESULT 5
 ID R37215 standard; Protein; 468 AA.
 AC R37215; 1993 (first entry)
 DT 13-SEP-1993 (first entry)
 DE IL-6 receptor.
 KW Interleukin-6; IL-6; receptor; immunoglobulin-like; domain; truncated;
 KW transmembrane; multiple myeloma; binding; ability; signal transfer;
 KW disease; intracellular.
 OS Synthetic.
 PN J05091892-A.
 PD 16-APR-1993.
 PF 02-OCT-1991; 255521.
 PR 02-OCT-1991; JP-255521.
 PA (CHUS) CHUGAI PHARM CO LTD.
 PA (KISH/) KISHIMOTO C.
 PA (TOI)) TOSOH CORP.
 DR WPI; 93-161739/20.
 DR N-PSDB; Q41746.
 PT New interleukin-6 receptor deriv. - for treating diseases caused
 PT by IL-6, e.g. multiple myeloma
 PS Disclosure; Page 10-12; 23pp; Japanese.
 CC This sequence represents an interleukin-6 (IL-6) receptor. Variants
 CC of the receptor lacking either the immunoglobulin-like domain or the
 CC transmembrane and intracellular domain have IL-6 binding ability and
 CC signal transfer ability. Either the full length or truncated IL-6
 CC receptors may be used for diseases caused by IL-6 such as multiple
 CC myeloma.
 SQ Sequence 468 AA;

Query Match 63.6%; Score 2398; DB 1; Length 468;

Best Local Similarity 100.0%; Pred. No. 3.10e-185;		
Matches	323; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Db	1	MLAVGCALLAALLAAPGAALAPRRCPAQEYARGVLTSLPGDSVTLTCTCPGVEPEDNATVHW 60
Qy	1	MLAVGCALLAALLAAPGAALAPRRCPAQEYARGVLTSLPGDSVTLTCTCPGVEPEDNATVHW 60
Db	61	VLRPAAGSHPSRWAGMGRLLRLRSVOLHDSGNSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
Qy	61	VLRPAAGSHPSRWAGMGRLLRLRSVOLHDSGNSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
Db	121	CFRKSPLSNVCEWGPBPSLTTKAVLLYRKFNQSPAEDFQPCQYSOESOKFSCQLAV 180
Qy	121	CFRKSPLSNVCEWGPBPSLTTKAVLLYRKFNQSPAEDFQPCQYSOESOKFSCQLAV 180
Db	181	PEGDSFFIYIVSMCVASSVSGSKFSTQTFQCGILQDPDPANITVTAVARNPRLSVTWQD 240
Qy	181	PEGDSFFIYIVSMCVASSVSGSKFSTQTFQCGILQDPDPANITVTAVARNPRLSVTWQD 240
Db	241	PHSNNSFYRLRELRYRAERSKFTFTTMVKDLOHHCVIDHAWSGLRHVYVQLRAQEEFGQ 300
Qy	241	PHSNNSFYRLRELRYRAERSKFTFTTMVKDLOHHCVIDHAWSGLRHVYVQLRAQEEFGQ 300
Db	301	GEWSEWSPKAMGTPWTESRPPA 323
Qy	301	GEWSEWSPKAMGTPWTESRPPA 323
RESULT	6	
ID	AC	P90284 standard; Protein; 468 AA.
DE	31-MAR-1992	(first entry)
DE		Sequence of a receptor protein for human B cell stimulating
DE		factor-2 (BSF2 receptor).
OS		B cell; immune disorder; therapy; diagnosis; prophylaxis.
OS		Homo sapiens.
FH	Key	Location/Qualifiers
FT	region	2..22
FT	region	/label= hydrophobic region
FT	region	362..386
FT	region	/label= hydrophobic region
PN		EP-325474-A.
PD		26-JUL-1989.
PF		20-JAN-1989; 300536.
PR		22-JAN-1988; JP-012387.
PR		25-JAN-1988; JP-012599.
PR		04-AUG-1988; JP-194885.
PR		14-JAN-1989; JP-017461.
PR		20-JAN-1989; JP-009774.
PA		(KISH/) KISHIMOTO T.
PI		Kishimoto T.
DR		WPI: 89-214667/30.
DR		N-PSDB; N90340.
PT		Receptor protein for human B cell stimulating factor-2 - obt'd. by
PT		recombinant DNA techniques and used as diagnostic, prophylactic or
PT		therapeutic agent
PS		Claim 2; Page 19-21; 63pp; English.
CC		The cDNA in N90340 was derived from monocyte cell line U937.
CC		Isolated BSF2 receptor and DNA encoding it are claimed, as are
CC		(b) expression vectors; (c) host organisms; (d) antibodies; and
CC		(e) hybridomas.
SQ		Sequence 468 AA:

	Query Match	63.6%	Score 2398;	DB 1;	Length 468;
	Best Local Similarity 100.0%;		Pred. No. 3.10e-185;		
	Matches 323;	Conservative 0;	Indels 0;	Gaps 0;	
Db	1	MLAVGCALLAALLAAPGAALAPRC	PAQEVARGVLTSLPGDSVTLTCG	VEPEDNATVHW	60
Qy	1	MLAVGCALLAALLAAPGAALAPRC	PAQEVARGVLTSLPGDSVTLTCG	VEPEDNATVHW	60
Db	61	YLKFAAGCHSRVWAGMGRLLLSRV	QLHDSGNTSCYTRAGPRAGTVHLL	VDVPPPEQLS	120

QY	61	VLRPAAGSHPSRWAGMGRLLRLLSVQLHDSGNYSCYRAGRAGTGVHLLVDVPPPEPQLS	120
Db	121	CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQSPCOYSOESQKFSQOLAV	180
QY	121	CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQSPCOYSOESQKFSQOLAV	180
Db	181	PEGDSFYIVSMCVASSVSGSKFSTQTFQCGILQDPDPANITVTAVARNRWLSVTWQD	240
QY	181	PEGDSFYIVSMCVASSVSGSKFSTQTFQCGILQDPDPANITVTAVARNRWLSVTWQD	240
Db	241	PHSNNSFYRLRFELRYRAERSTFTTMVKDQLQHCVTHDAWSGLRHVVQLRAQEEFGQ	300
QY	241	PHSNNSFYRLRFELRYRAERSTFTTMVKDQLQHCVTHDAWSGLRHVVQLRAQEEFGQ	300
Db	301	GEWSEWPEAWGTPWTESRPPA	323
QY	301	GEWSEWPEAWGTPWTESRPPA	323
RESULT	7		
ID	AC	W70804 standard; protein; 360 AA.	
ID	AD	W70804;	
DT	03-FEB-1999	(first entry)	
DE		Amino acid sequence of the interleukin (IL)-6R-alpha domain.	
KW	gpl30; cytokine antagonist; interleukin; gamma-interferon;		
KW	granulocyte macrophage colony-stimulating factor; J peptide;		
KW	transforming growth factor-beta.		
KS	Synthetic.		
KEY	Key	Location/Qualifiers	
FT	FT	I. .358	
FT	FT	/note= "soluble interleukin (IL)-6R-alpha domain"	
PN	PN	US5844099-A.	
PD	PD	01-DEC-1998.	
PF	PF	27-NOV-1995; 563105.	
PR	PR	27-NOV-1995; US-563105.	
PR	PR	20-OCT-1993; US-140222.	
PA	PA	(REGE-) REGENERON PHARM INC.	
PI	PI	Economides A, Stahl N, Yancopoulos GD;	
DR	DR	WPI; 99-044669/04.	
PT	PT	Cytokine antagonists - comprising extracellular domains of	
PT	PT	specificity-determining and signal-transducing components of	
PT	PT	cytokine receptor	
PS	PS	Example 4; Fig 15; 46pp; English.	
CC	CC	The present sequence represents the amino acid sequence of interleukin	
CC	CC	(IL)-6R-alpha domain. The protein is used in the course of the invention.	
CC	CC	The specification describes cytokine antagonists comprising only the	
CC	CC	extracellular domain of the specificity-determining component of	
CC	CC	the cytokine receptor and the extracellular domain of a	
CC	CC	signal-transducing component of the cytokine receptor. The cytokine	
CC	CC	is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),	
CC	CC	granulocyte macrophage colony-stimulating factor (GM-CSF),	
CC	CC	gamma-interferon or transforming growth factor-beta (TGF-beta). The	
CC	CC	antagonist is capable of binding the cytokine to form a nonfunctional	
CC	CC	complex. The compounds have therapeutic activity as cytokine antagonists	
CC	CC	and can also be used in assays for identifying novel agonists and	
CC	CC	antagonists of cytokines.	
CC	CC	Sequence 360 AA;	
QY	Query Match	63.4%; Score 2391; DB 1; Length 360;	
DB	Best Local Similarity	99.7%; Pred. No. 1.19e-184;	
Matches	322; Conservative	1; Mismatches 0; Indels 0; Gaps 0;	

	Db	1	MVAVGALLAALLAAPGAALAPRRCPAQEVARGVLTSIPGDSVTLTTCGPVEPDNATVHW : : :	60
	QY	1	MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSIPGDSVTLTTCGPVEPDNATVHW 	60
	Db	61	VLRKPAAGSHPSRWAGMGRLLRSVLHDSGNYSCTYRAGRPAGTVHLHYDVDPPEEPQLS 	120
	QY	61	VLRKPAAGSHPSRWAGMGRLLRSVLHDSGNYSCTYRAGRPAGTVHLHYDVDPPEEPQLS 	120
	Db	121	CFRKSPLSNVCEWGPSTPSLTKVALLVRKFONSPAEDFQBPQYSQSBSKFSCOLAV 	180
	QY	121	CFRKSPLSNVCEWGPSTPLTTKVALLVRKFONSPAEDFQBPQYSQSBSKFSCOLAV 	180

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Db      301 GEWSEWSP EAMGTPWTESRSPPA 323
      |||||
QY      301 GEWSEWSP EAMGTPWTESRSPPA 323

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RESULT	10	
ID	W70797	standard; protein; 592 AA.
AC	W70797;	
DT	03-FEB-1999	(first entry)
DE	Human interleukin-6R-alpha-Fc.	
KW	gpl30; cytokine antagonist; interleukin; gamma-interferon;	
KW	granulocyte macrophage colony-stimulating factor; J peptide;	
KW	transforming growth factor-beta.	
OS	Synthetic.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	Protein	1..358
FT		/note= "human IL-R-alpha"
FT	Misc_difference 2	
FT		/label= L2V

FT Peptide /note= "changed to accomodate a kozak sequence"
 FT 1. .19
 FT /note= "signal peptide"
 FT Misc_difference 359. .360
 FT /note= "Ala-Gly bridge"
 FT Protein 361. .562
 FT /note= "Fc domain of human IgG1"
 FT Disulfide_bond 371. .374
 PN US5844099-A.
 PD 01-DEC-1998.
 PF 27-NOV-1995; 563105.
 PR 27-NOV-1995; US-563105.
 PR 20-OCT-1993; US-140222.
 PA (REGG-) REGENERON PHARM INC.
 PI Economides A, Stahl N, Yancopoulos GD;
 DR WPI; 99-044669/04.
 PR Cytokine antagonists - comprising extracellular domains of
 PT specificity-determining and signal-transducing components of
 PT cytokine receptor
 PS Example 3; Fig 5; 46pp; English.
 CC The present sequence represents the amino acid sequence of human
 CC interleukin (IL)-6R-alpha-Fc. The protein is used in the course
 CC of the invention. The specification describes cytokine antagonists
 CC comprising only the extracellular domain of the specificity-determining
 CC component of the cytokine receptor and the extracellular domain of a
 CC signal-transducing component of the cytokine receptor. The cytokine
 CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
 CC granulocyte macrophage colony-stimulating factor (GM-CSF),
 CC gamma-interferon or transforming growth factor-beta (TGF-beta). The
 CC antagonist is capable of binding the cytokine to form a nonfunctional
 CC complex. The compounds have therapeutic activity as cytokine antagonists
 CC and can also be used in assays for identifying novel agonists and
 CC antagonists of cytokines.
 SQ Sequence 592 AA;

Query Match 63.4%; Score 2391; DB 1; Length 592;
 Best Local Similarity 99.7%; Pred. No. 1.19e-184;
 Matches 322; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 1 MVAVCALLAALLAAGAAAPRRCPAQEVARGVLTSLPGDSVLTCPGVPEPNATVHW 60
 Qy 1 MLAVGCALLAALLAAGAAAPRRCPAQEVARGVLTSLPGDSVLTCPGVPEPNATVHW 60
 Db 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNTSCYRAGRPAGTVHLLVDVPPPEPOLS 120
 Qy 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNTSCYRAGRPAGTVHLLVDVPPPEPOLS 120
 Db 121 CFRKSPLSNVVCEWGPRTSLTTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFSQOLAV 180
 Qy 121 CFRKSPLSNVVCEWGPRTSLTTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFSQOLAV 180
 Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQPDPPANITVAVARNPRLSVTWQD 240
 Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQPDPPANITVAVARNPRLSVTWQD 240
 Db 241 PHSNSSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDANSGLRHVVQLRAQEEFGQ 300
 Qy 241 PHSNSSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDANSGLRHVVQLRAQEEFGQ 300
 Db 301 GEWSESPAMGTPWTSRSPPA 323
 Qy 301 GEWSESPAMGTPWTSRSPPA 323

RESULT 11
 ID W71371 standard; Protein; 468 AA.
 AC W71371;
 DT 02-FEB-1999 (first entry)
 DE Human interleukin-6 receptor alpha polypeptide.
 KW Interleukin-6 receptor; human; hepatitis B virus; HBV; infection;
 SW therapy.
 OS Homo sapiens.
 PN WO9835694-A2.

PD 20-AUG-1998.
 PF 10-FEB-1998; U08898.
 PR 11-FEB-1997; US-795473.
 PA (DAVI/) DAVIDSON C M.
 PR (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
 DR WPI; 98-520755/44.
 PT Treatment of hepatitis B virus infection - using a soluble active
 PT agent which prevents interaction of HBV with hepatocytes mediated by
 PT human interleukin 6
 PS Disclosure; Fig 9; 51pp; English.
 CC This is a previously reported amino acid sequence for human
 CC interleukin-6 (hIL-6) receptor alpha. The invention relates to
 CC the finding that hIL-6 is essential for hepatitis B virus (HBV)
 CC infection. The invention provides a pharmaceutical composition for
 CC the treatment of HBV infection, comprising a soluble active agent
 CC that interacts with at least one of the binding sites between hIL-6
 CC and the psi region of HBV and between hIL-6 and hepatocytes and
 CC other HBV-permissive cells. The active agent competitively binds
 CC to at least one of these sites and thereby prevents hIL-6-mediated
 CC HBV infection of hepatocytes and other HBV-permissive cells. The
 CC soluble active agent is selected from glycoprotein 80 (gp80) having
 CC receptor sites which interact with hIL-6, soluble glycoprotein 130
 CC (gp130) having receptor sites which interact with hIL-6, hIL-6
 CC derived peptide Lys41-Ala56, hIL-6 derived peptide Gly77-Glu95,
 CC hIL-6 derived peptide Gln153-His165, a combined 1 and 2 hIL-6
 CC mutant (mhIL-6 1+2), and mhIL-6 1+2 substituted with Phe171 to Leu
 CC and Ser177 to Arg, and mixtures of any of these.
 SQ Sequence 468 AA;

Query Match 62.9%; Score 2373; DB 1; Length 468;
 Best Local Similarity 99.1%; Pred. No. 3.83e-183;
 Matches 320; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Db 1 MLAVGCALLAALLAAGAAAPRRCPAQEVARGVLTSLPGDSVLTCPGVPEPNATVHW 60
 Qy 1 MLAVGCALLAALLAAGAAAPRRCPAQEVARGVLTSLPGDSVLTCPGVPEPNATVHW 60
 Db 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNTSCYRAGRPAGTVHLLVDVPPPEPOLS 120
 Qy 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNTSCYRAGRPAGTVHLLVDVPPPEPOLS 120
 Db 121 CFRKSPLSNVVCEWGPRTSLTTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFSQOLAV 180
 Qy 121 CFRKSPLSNVVCEWGPRTSLTTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFSQOLAV 180
 Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQPDPPANITVAVARNPRLSVTWQD 240
 Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQPDPPANITVAVARNPRLSVTWQD 240
 Db 241 PHSNSSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDANSGLRHVVQLRAQEEFGQ 300
 Qy 241 PHSNSSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDANSGLRHVVQLRAQEEFGQ 300
 Db 301 GEWSESPAMGTPWTSRSPPA 323
 Qy 301 GEWSESPAMGTPWTSRSPPA 323

RESULT 12
 ID P90527 standard; protein; 323 AA.
 AC P90527;
 DT 25-JAN-1990 (first entry)
 DE B cell stimulating factor-2 receptor.
 KW B cell stimulating factor-2 receptor; monocyte U937 cell line.
 OS Homo sapiens.
 PN AU8928720-A.
 PD 27-JUL-1989.
 PF 23-JAN-1989; 28720.
 PR 22-JAN-1988; JP-012387.
 PR 25-JAN-1988; JP-012599.
 PR 04-AUG-1988; JP-194885.
 PR 14-JAN-1989; JP-007461.
 PA (KISH) Tadimitsu Kishimoto.

PI Kishimoto T;
DR WPI: 89-264012/37.
DR N-P5DB; P90525.
PT Receptor protein for human B cell stimulating factor-2 - used for
PT developing prophylactic, therapeutic and diagnostic agents for
PT associated disorders.
PS Claim 6; page 39; 76pp; english.
CC The BSF2 receptor has amino acids at the C-terminal deleted. The receptor
CC is derived from a monocytic U937 cell line. It can be used to develop
CC prophylactic and therapeutic pharmaceuticals, as agents to relate
CC diseases and disorders to abnormal BSF-2 prodn. It can also be used to
CC study an immune mechanism with which BSF-2 or the receptor is concerned.
SQ Sequence 323 AA;

Query Match 62.3%; Score 2351; DB 1; Length 323;
Best Local Similarity 98.8%; Pred. No. 2.66e-181;
Matches 318; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1 MIAVGCALLAALAPGAALAPRCAPAEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
QY 1 MIAVGCALLAALAPGAALAPRCAPAEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

Db 61 VLKPPAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRAGTGHLLVDVPPPEPQLS 120
QY 61 VLKPPAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRAGTGHLLVDVPPPEPQLS 120

Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLYRKFNQSPAEDEFQPCQYSQESKFSCQLAV 180
QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLYRKFNQSPAEDEFQPCQYSQESKFSCQLAV 180

Db 181 PEGDSFYIVSMCVASSVSGSKFSTQTQFCGGLQDPDPANITVAVARNRWLSVTWQD 240
QY 181 PEGDSFYIVSMCVASSVSGSKFSTQTQFCGGLQDPDPANITVAVARNRWLSVTWQD 240

Db 241 PHSWNSFYRLRFELRYAERSKFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEFGQ 300
QY 241 PHSWNSFYRLRFELRYAERSKFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEFGQ 300

Db 301 GGEWSEWSPAMGTPWTESRSP 322
QY 301 GGEWSEWSPAMGTPWTESRSP 322

RESULT 13
ID W70805 standard; protein; 315 AA.
AC W70805;
DT 03-FEB-1999 (first entry)
DE Amino acid sequence of the interleukin (IL)-6R-alpha-313 domain.
KW gp130; cytokine antagonist; interleukin; gamma-interferon;
KW granulocyte macrophage colony-stimulating factor; J peptide;
KW transforming growth factor-beta.
OS Synthetic.
FH Key Location/Qualifiers
FT 1..313 /note= "truncated interleukin (IL)-6R-alpha domain"
FT US5844099-A.
PN 01-DEC-1998.
PD 27-NOV-1995; 563105.
PR 27-NOV-1995; US-563105.
PR 20-OCT-1993; US-140222.
PA (REG-) REGENERON PHARM INC.
PI Economides A, Stahl N, Yancopoulos GD;
DR WPI: 99-044669/04.
PT Cytokine antagonists - comprising extracellular domains of
PT specificity-determining and signal-transducing components of
PT cytokine receptor
PS Example 4; Fig 16; 46pp; English.
CC The present sequence represents the amino acid sequence of interleukin
CC (IL)-6R-alpha-313 domain. The protein is used in the course of the
CC invention. The specification describes cytokine antagonists comprising
CC only the extracellular domain of the specificity-determining component of
CC the cytokine receptor and the extracellular domain of a
CC signal-transducing component of the cytokine receptor. The cytokine

CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
CC granulocyte macrophage colony-stimulating factor (GM-CSF),
CC gamma-interferon or transforming growth factor-beta (TGF-beta). The
CC antagonist is capable of binding the cytokine to form a nonfunctional
CC complex. The compounds have therapeutic activity as cytokine antagonists
CC and can also be used in assays for identifying novel agonists and
CC antagonists of cytokines.
SQ Sequence 315 AA;

Query Match 61.4%; Score 2317; DB 1; Length 315;
Best Local Similarity 99.7%; Pred. No. 1.86e-178;
Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MIAVGCALLAALAPGAALAPRCAPAEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
QY 1 MIAVGCALLAALAPGAALAPRCAPAEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

Db 61 VLKPPAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRAGTGHLLVDVPPPEPQLS 120
QY 61 VLKPPAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRAGTGHLLVDVPPPEPQLS 120

Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLYRKFNQSPAEDEFQPCQYSQESKFSCQLAV 180
QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLYRKFNQSPAEDEFQPCQYSQESKFSCQLAV 180

Db 181 PEGDSFYIVSMCVASSVSGSKFSTQTQFCGGLQDPDPANITVAVARNRWLSVTWQD 240
QY 181 PEGDSFYIVSMCVASSVSGSKFSTQTQFCGGLQDPDPANITVAVARNRWLSVTWQD 240

Db 241 PHSWNSFYRLRFELRYAERSKFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEFGQ 300
QY 241 PHSWNSFYRLRFELRYAERSKFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEFGQ 300

Db 301 GGEWSEWSPAMGT 313
QY 301 GGEWSEWSPAMGT 313

RESULT 14
ID R70122 standard; Protein; 1042 AA.
AC R70122;
DT 14-FEB-1996 (first entry)
DE IL8-R type 1-GBP 130 fusion protein.
KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A.
OS Chimeric Homo sapiens.
OS Chimeric Plasmodium falciparum.
FH Key Location/Qualifiers
FT misc_difference 54 /label= OTHER
FT W09506737-A.
PN 09-MAR-1995.
PD 01-SEP-1994; G01900.
PR 03-SEP-1993; GB-018350.
PR 23-AUG-1994; GB-017021.
PA (PREN/) PRENDERGAST K F.
PI Prendergast KF;
DR WPI: 95-115452/15.
PT New hybrid peptide(s) for binding cytokine(s) - comprising a
PT malaria parasite peptide capable of binding a red blood cell and
PT a receptor peptide.
PS Example A; Page 77-78; 93pp; English.
CC Hybrid peptides for binding cytokines, comprising a malaria parasite
CC (Plasmodium falciparum) peptide (capable of binding to a red blood
CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC of these hybrid peptides. R70122 is a fusion of interleukin 6 receptor
CC (as confirmed with reference to SWISSPROT, as it is unclear in the
CC specification whether this sequence is IL8-R or IL8-R type) and
CC glycophorin binding protein (GBP) 130. The use of cytokine receptors not
CC normally found on RBCs means that the cytokine can bind harmlessly to the
CC RBC without deleterious effect. The RBC protects the hybrid peptides from

CC excretion from the kidney, and due to steric hindrance prevents the
 CC cytokines binding to a receptor in another cell. GBP 130 or GBPH
 CC (GBP homologue) are the prefid. malaria parasite peptides used, others
 CC include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA (pre major
 CC merozoite surface antigen) and the Duffy binding receptor molecule (eg.
 CC exhibited by Plasmodium vivax). These peptides bind to pref. glycoprotein
 CC A, B and C, sialo glycoproteins, found on the surface of RBCs. The hybrid
 CC peptides are thus used to lower the levels of free cytokines in the
 CC circulation to reduce pathological damage.
 SQ Sequence 1042 AA;

Query Match 56.0%; Score 2110; DB 1; Length 1042;
 Best Local Similarity 97.0%; Pred. No. 3.77e-161;
 Matches 295; Conservative 0; Mismatches 1; Indels 8; Gaps 2;

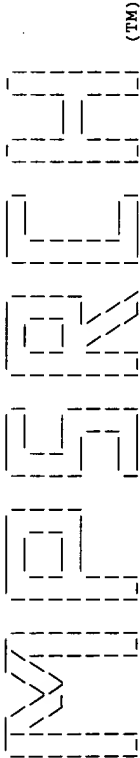
Db 1 LAPRCRPAQEVARGVLTSLPGDSTVLTCPGVEPEDNATVHVLRKPAAGSHPSXWAGNGR 60
 QY 20 LAPRCRPAQEVARGVLTSLPGDSTVLTCPGVEPEDNATVHVLRKPAAGSHPSXWAGNGR 79
 Db 61 RLLRSVLHDSGNYSY-AGRPAGTTHLLVDVPPPEPQLSCFRKSPLSNVVCEWGPST 119
 QY 80 RLLRSVLHDSGNYSYRAGRAGTTHLLVDVPPPEPQLSCFRKSPLSNVVCEWGPST 139
 Db 120 PSLTFTKAVLLVRKFNQSPAEFQ-----SQFSCQLAVPEGDSFYIVSMCVASSVG 172
 QY 140 PSLTFTKAVLLVRKFNQSPAEFQ-----SQFSCQLAVPEGDSFYIVSMCVASSVG 199
 Db 173 SKFSKTQFGCGILQDPDPANITVAVARNRPLSVTWQDPHNSWNSFYRLRFLRYRA 232
 QY 200 SKFSKTQFGCGILQDPDPANITVAVARNRPLSVTWQDPHNSWNSFYRLRFLRYRA 259
 Db 233 ERSKTFTTMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGGSEWSEPEAMGTPWTESR 292
 QY 260 ERSKTFTTMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGGSEWSEPEAMGTPWTESR 319
 Db 293 SPPA 296
 QY 320 SPPA 323

RESULT 15
 ID P0526 standard; protein; 386 AA.
 AC P0526; 1990 (first entry)
 DT 25-JAN-1990 (first entry)
 DE B cell stimulating factor-2 receptor.
 KW B cell stimulating factor-2 receptor; monocytic U937 cell line.
 OS Homo sapiens.
 PN A08928720-A.
 PD 27-JUL-1989.
 PF 23-JAN-1989; 28720.
 PR 22-JAN-1988; JP-012387.
 PR 25-JAN-1988; JP-012599.
 PR 04-AUG-1988; JP-194885.
 PR 14-JAN-1989; JP-007461.
 PA (KISH) Tadamoto Kishimoto.
 PI Kishimoto T;
 DR WPI; 89-264012/37.
 DR N-PSDB; P90525.
 PT Receptor protein for human B cell stimulating factor-2 - used for
 PT developing prophylactic, therapeutic and diagnostic agents for
 PT associated disorders.
 PS Claim 4; page 37-8; 76pp; english.
 CC The BSF2 receptor has residues near the N-terminal deleted. The receptor
 CC is derived from a monocytic U937 cell line. It can be used to develop
 CC prophylactic and therapeutic pharmaceuticals as agents to relate diseases
 CC and disorders to abnormal BSF-2 prodn. It can also be used to study an
 CC immune mechanism with which BSF-2 or the receptor is concerned.
 SQ Sequence 386 AA;

Query Match 40.7%; Score 1534; DB 1; Length 386;
 Best Local Similarity 97.7%; Pred. No. 3.78e-113;
 Matches 211; Conservative 0; Mismatches 1; Indels 4; Gaps 2;

Db 28 VDVPEPQLSCFRKSPLSNVVC--GPRSTPEWSITTKAVLLVRKFNQSPAEFQEPQY 85
 QY 110 VDVPEPQLSCFRKSPLSNVVCEWGPSTP--SLTTKAVLLVRKFNQSPAEFQEPQY 167
 Db 86 SQESQKFSQCLAVPEGDSFYIVSMCVASSVGSFSTQTFQCGGILQDPDPANITVAV 145
 QY 168 SQESQKFSQCLAVPEGDSFYIVSMCVASSVGSFSTQTFQCGGILQDPDPANITVAV 227
 Db 146 ARNPRWLSVTWQDPHNSWNSFYRLRFLRYRAERSKTFTTMVKDLQHCVIHDAWSGLR 205
 QY 228 ARNPRWLSVTWQDPHNSWNSFYRLRFLRYRAERSKTFTTMVKDLQHCVIHDAWSGLR 287
 Db 206 HVVOLRAQEEFGGSEWSEPEAMGTPWTESRSPA 241
 QY 288 HVVOLRAQEEFGGSEWSEPEAMGTPWTESRSPA 323

Search completed: Thu Aug 10 16:13:25 2000
 Job time : 64 secs.



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Aug 10 16:28:58 2000; MasPar time 19.54 Seconds
Tabular output not generated. 752.058 Million cell updates/sec

Title: >US-09-142-471-5

Description: (1-212) from US09142471.pep

Perfect Score: 1485

Sequence: 1 MNSFSTSAFGVAFSLGILL.....LILSLKEFLQSLRALRQM 212

Scoring table: PAM 150

Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: sptrembl12

1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phase 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus

Statistics: Mean 45.366; Variance 84.647; scale 0.536

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description	Pred. No.
1	1382	93.1	209	6	INTERLEUKIN-6 (FRAGMENT)	5.72e-273
2	940	63.3	209	6	INTERLEUKIN 6 (FRAGMENT)	5.49e-174
3	915	61.6	160	6	INTERLEUKIN-6 (FRAGMENT)	1.93e-168
4	892	60.1	208	6	INTERLEUKIN 6 PRECURSOR	2.41e-163
5	891	60.0	205	6	INTERLEUKIN 6 (FRAGMENT)	4.02e-163
6	855	57.6	207	6	INTERLEUKIN 6 (FRAGMENT)	3.68e-155
7	613	41.3	210	11	IL-6 (FRAGMENT)	3.42e-102
8	377	25.4	94	6	INTERLEUKIN 6 (FRAGMENT)	3.65e-52
9	320	21.5	101	11	ORF K2	1.51e-40
10	256	17.2	204	14	INTERLEUKIN-6 (FRAGMENT)	6.83e-28
11	256	17.2	204	14	INTERLEUKIN-6 HOMOLOG	6.83e-28
12	126	8.5	194	6	GRANULOCYTE COLONY-STI	1.03e-04
13	119	8.0	656	2	HYPOTHETICAL 74.9 KD P	1.20e-03
14	113	7.6	207	14	INTERLEUKIN-6 HOMOLOG	9.18e-03
15	113	7.6	214	11	GRANULOCYTE COLONY STI	9.18e-03
16	112	7.5	589	5	PF20 HOMOLOG	1.28e-02
17	109	7.3	219	13	PROGLUCAGON II	3.45e-02
18	109	7.3	321	10	SYNTAXIN-LIKE PROTEIN	3.45e-02
19	107	7.2	251	2	O-ACETYL SERINE SYNTHAS	6.62e-02
20	106	7.1	266	13	PROGLUCAGON I	9.15e-02

21	105	7.1	3027	4	Q9Y485	X-LIKE 1 PROTEIN.	1.26e-01
22	103	6.9	494	5	Q9X2W0	GABA-GATED CHLORIDE CH	2.38e-01
23	101	6.8	314	10	Q43664	ANNEXIN P35.	4.47e-01
24	101	6.8	815	10	Q22113	HCR2.	4.47e-01
25	99	6.7	195	6	O19180	GRANULOCYTE-COLONY STI	8.30e-01
26	100	6.7	298	10	Q43455	HEAT SHOCK TRANSCRIPT	6.09e-01
27	100	6.7	496	5	O18468	GABA-GATED CHLORIDE CH	6.09e-01
28	99	6.7	780	11	Q60537	APOLIPOPROTEIN B (FRAG	8.30e-01
29	99	6.7	780	11	Q60536	APOLIPOPROTEIN (APOB)	8.30e-01
30	100	6.7	1099	10	Q9XK88	UNCONVENTIONAL MYOSIN	6.09e-01
31	99	6.7	1642	4	O14869	YOTIAO.	8.30e-01
32	100	6.7	1690	3	Q20937	PUTATIVE RNA BIOGENES	6.09e-01
33	99	6.7	2500	5	O74835	SIMILAR TO S.	8.30e-01
34	99	6.7	3899	4	Q9Y6Y2	CENTROSOME-AND GOLGI-L	8.30e-01
35	99	6.7	3911	4	Q99996	HYPERION PROTEIN (YOTI	8.30e-01
36	96	6.5	241	14	Q04161	PHOSPHOPROTEIN (FRAGME	2.07e+00
37	97	6.5	373	4	Q9Y2X6	ARFAPTTIN-1B.	1.53e+00
38	96	6.5	422	14	Q9WII5	GENE FOR THYMIDINE KIN	2.07e+00
39	96	6.5	759	14	Q67323	POLYMERASE.	2.07e+00
40	97	6.5	880	4	Q9Y4B0	P1.11659.3.	1.53e+00
41	96	6.5	1197	11	Q920F5	ESE2 PROTEIN.	2.07e+00
42	97	6.5	1419	5	Q45092	F58H7 6 PROTEIN.	1.53e+00
43	96	6.5	1658	11	Q9Z0R6	ESE2L PROTEIN.	2.07e+00
44	97	6.5	1938	6	Q28641	MYOSIN HEAVY CHAIN.	1.53e+00
45	95	6.4	241	14	Q42062	PHOSPHOPROTEIN.	2.79e+00

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	209 AA.
ID	Q9Y540			
AC	Q9Y540;			
DT	01-MAY-1999 (TREMBLrel. 10, Created)			
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)			
DE	INTERLEUKIN-6 (FRAGMENT).			
GN	IL-6.			
OS	Aekaryota; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	ECHEVERRY S.J., HERNANDEZ E., MORENO A., PATARROYO M.E., MURILLO L.A.;			
RT	"Identification, cloning and sequencing of different interleukin genes			
RT	in 4 Aotus species."			
RL	Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF014510; AAD01536.1; -			
DR	HSSP; P05231; IALU.			
DR	PROSITE; PS00254; INTERLEUKIN_6; 1.			
FT	NON_TER 1 1			
FT	NON_TER 209 209			
SQ	SEQUENCE 209 AA; 23406 MW; 99D77053 CRC32;			

Query Match	93.1%	Score 1382; DB 6; Length 209;
Best Local Similarity	94.3%;	Pred. No. 5.72e-273;
Matches	197; Conservative	8; Mismatches 4; Indels 0; Gaps 0;
Db	1 MNSFSTSAFGVAFSLGILLVMPAAPPVPPGSDSKEVAAPNPQPLTSTEQIDKHIRYI 60	
QY	1 MNSFSTSAFGVAFSLGILLVMPAAPPVPPGSDSKEVAAPNPQPLTSTEQIDKHIRYI 60	
Db	61 LDGISALRKETCNKSNCESSKEALNNLNPMAKDCGCFQSGFNEETCLVKIITGLL 120	
QY	61 LDGISALRKETCNKSNCESSKEALNNLNPMAKDCGCFQSGFNEETCLVKIITGLL 120	
Db	121 EFVYLEYLQNRFESESEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQ 180	
QY	121 EFVYLEYLQNRFESESEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQ 180	
Db	181 AQNWLODMTHLILRSKFELQSLRAL 209	
QY	181 AQNWLODMTHLILRSKFELQSLRAL 209	

RA	SPOTT J L., FERRICK D.A.:
RT	"Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT	the harbor seal (<i>Phoca vitulina</i>), killer whale (<i>Orcinus orca</i>), and
RT	Southern sea otter (<i>Ehndyra lutris nereis</i>).";
RL	Immunogenetics 43:190-195(1996).
DR	EMBL; L46803; AAB01429.1; -.
DR	HSSP; P05231; IALUJ
DR	PROSITE; PS00254; INTERLEUKIN_6; 1.
DR	PFAM; PF00489; IL-6; 1.
FT	NON_TER 1
SQ	SEQUENCE 205 AA; 23266 MW; C853C8DF CRC32;
	Query Match 60.0%; Score 891; DB 6; Length 205;
	Best Local Similarity 61.8%; Pred. No. 4.02e-163;
	Matches 123; Conservative 38; Mismatches 37; Indels 1; Gaps 1;
Dbb	5 AFSLGILLVTATAPPTGGPGEDFKDDTTSDRIYLYTSPOKTEALIKYLIGKISAMRKMC 64
QY	: : :: : : : : :
QY	13 AFSLGILLVLPAAFPAPVPGEESKDVAAPHROPLTSSERIDKOIRIYILDGISALKETC 72
Dbb	65 EKYDKCKENSKAELNINLPKNAEKDGCFCSGFNQETCLMRITTTGLLVEIYLDVLQNE 124
QY	: : : : : : : : : : : : : : :
QY	73 NKNMGCESSPEALAEINLNPKNKAEDKGCFSGFNDETCLVKITGLLEFEVYLEYLNQR 132
Dbb	125 YEGDKCAIEAVYSKKALAQLRQYKNPNDEVTTPDTTNASLMNNLQSONDDMKNTKI 184
QY	:: : : : : : : : : : : : : : :
QY	133 FESSEEQARAVQNSTKVLIQFLQKAKNLDAITTPDTTNASLLTKLQAQNQ-WLEDMP 191
Dbb	185 ILILRSLENLFQSRLAIR 203
QY	: : : : : : : : : : : : :
QY	192 HLILSRKEFLQRSRLAIR 210

RESULT		6			
ID	Q28403		PRELIMINARY;	PRT;	207 AA.
AC	Q28403;				
DT	01-NOV-1996	(TREMBLREL_01,	Created)		
DT	01-NOV-1996	(TREMBLREL_01,	Last sequence update)		
DE	01-NOV-1999	(TREMBLREL_12,	Last annotation update)		
DT	INTERLEUKIN 6	{FRAGMENT}.			
GN	IL-6.				
OS	Euhadra lutris	(Sea otter).			
OC	Eukaryota; Metazoa;	Chordata; Craniata;	Vertebrata; Mammalia;		
RN	Eutheria; Carnivora;	Fissipedia; Mustelidae;	Enhydra.		
RC	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE:	96163018.			
RA	KING D.P., SCHRENZEL M.D.,	MCKNIGHT M.L., REIDARSON T.H., HANNI K.D.,			
RA	STOTT J.L., FERRICK D.A.;				
RT	"Molecular cloning and sequencing of interleukin 6 cDNA fragments from				
RT	the harbor seal (<i>Phoca vitulina</i>), killer whale (<i>Orcinus orca</i>), and				
RT	Southern sea otter (<i>Euhadra lutris nereis</i>).";				
RL	Immunogenetics 43:190-195(1996)."				
RL	EMBL: L46804; AAB01428.1;	-			
DR	HSSP: P05231;	2IL6			
DR	PROSITE: PS00254;	INTERLEUKIN_6;	1.		
DR	PFAM: PF00489;	IL-6;	1.		
FT	NON_TER		1		
SF	SEQUENCE	207 AA;	23527 MW;	OF2CAG62 CRC32;	

Query Match	57.6%	Score 855;	DB 6;	Length 207;
Best Local Similarity	56.74;	pred. No. 3.68e-155;		
Matches 118;	Conservative 46;	Mismatches 42;	Indels 2;	Gaps 2;
Db	2	STSAFSPVAFSLGILLVMTAFPTPGLCGDSKDDATSNRPPLTSSADKWEDFIKFLGI	61	
		: : :	: : :	
QY	5	STSAFSPVAFSLGILLVLPAAFPAPVPYPPGDSKDVAAHPHQRPILTSSERIDKQIRYILDI	64	
		: : :	: : :	
Db	62	SALRNEMCDKYNCKDSKEVLAEANNLNLPLAEKDKCFOSRFRNQETCLTRITTGLOEFOI	121	
		:	: : :	
QY	65	SALRKETCNKSNWCSSPEALAEANNLNLPKMAEKOCGCFOSGFNEETCLVKILITGLLEFEV	124	
		: : :	: : :	
Db	122	HLKYLSENYEGNKDNHAHSYISTKHLLQTLRPM-NQIE-VTPDPDPTDASLQALFKSODK	179	

```

| |||| :||: :||: :||: | ||: | : : : |||||: || : : |:
QY 125 YLEYLQRFFESSEQARAVOMSTKVLIQFLQKAKNLDATTPDTTNASLLTKLAQNQ 184
Db 180 WLKHHTTHLILRLLEDFLOFSRAIRM 207
QY 185 WLEDMPHLLIURLSKEFQLSRALROM 212
||||| :||: :||: :||: | ||: | : : : |||||: || : : |:

RESULT 7
ID Q9WV08 PRELIMINARY; PRT; 210 AA.
AC Q9WV08;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE IL-6 (FRAGMENT).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN-APA; TISSUE-KIDNEY;
RA NISHIDA E.;
RT "APA hamsters Il-6 partial cDNA.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB028635; BAA78766.1; -.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ NON_TER 1
SEQUENCE 210 AA; 24060 MW; 0307F113 CRC32;

```

Query Match 41.3%; Score 613; DB 11; Length 210;
Best Local Similarity 39.5%; Pred. No. 3.42e-102;
Matches 83; Conservative 58; Mismatches 65; Indels

Db	2	LSARDFHPLVF - LGLLLVATAALPTSOVRGRDFTD - TTPNPVYVYTSQVGGVLTVYVL	59
Qy	4	FSTSAFGVAFSLGLLLVLPAAFPAP - VPPGDSKVAAPHROPLTSSERIDKQIRYLD	62
Db	60	EIYELRELGNPNPGCMNDYVLENNLELPVIOINDGCLOTGYNWEICLLKITSGLLDY	119
Qy	63	GISALRKETCNKSMCESSPEALAEANLNLPKWAEDKQFCQSGFNETCLVLIITGLLF	122
Db	120	QIYLEFVTVNNQNDKKARVIOSTIKTLSPKQEVKPGDKTVTPSTPSKAILMEKLES	179
Qy	123	EVLYEYLQNR - ESSEBQARQVMSIKVLQFLQKAKAKNLDAITTPDPTTNASLLKQLA	181
Db	180	QKEWPRKTKLILKALEEFLEVTVMRSTRQ	209
Qy	182	QNWLEDMPTHILRSKLEFQSRSLRQ	211

RESULT		8		
ID	O62775		PRELIMINARY;	PRT; 94 AA.
AC	O62775;			
DT	01-AUG-1998	(TREMBLrel. 07, Created)		
DT	01-AUG-1998	(TREMBLrel. 07, Last sequence update)		
DT	01-NOV-1999	(TREMBLrel. 12, Last annotation update)		
DE	INTERLEUKIN 6 (FRAGMENT).			
OS	Felis silvestris catus (Cat).			
OC	Eukaryota; Metazoa; Chordata;			
OC	Aurynia; Carnivora; Fissipedia; Felidae; Felis.			
OC	Mammalia; Mammalia;			

[1] SEQUENCE FROM N.A.
HARLEY R., HELPS C.R., GRUFFYDD-JONES T.J., DAY M.J., HARBOUR D.A.;
Submitted (MAR-1998) to the EMBL/Genbank/DDBJ databases.

EMBL; AF054603; AAC15976.1; -;
HSSP; P05231; 2IL6.

PFAM; PF00489; IL-6; 1.
NON_TER 1 1

SEQUENCE 94 AA; 11099 MW; 835867E6 CRC32;

Query Match . 25.4%; Score 377; DB 6; Length 94;
Best Local Similarity 48.9%; pred. No. 3.65e-52;
Matches 46; Conservative 21; Mismatches 27; Indels

[illegible]

RESULT 9
ID O55041 PRELIMINARY; PRT; 101 AA;

DT 01-JUN-1998 (TREMUREL. 06, Created)
DT 01-JUN-1998 (TREMUREL. 06, Last sequence update)
DT 01-NOV-1999 (TREMUREL. 12, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.

OS *Cricetulus griseus* (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; *Cricetulus*.
[1]
RN
RP SEQUENCE FROM N.A.

RA HEINE H., DELUDE R.D., MONKS B., GOLENBOCK D.T.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF044667; AAC02100.1; -.
DR HSSP; P05231; 2IL6.

DR PROSITE; PS00254; INTER
DR PFAM; PF00489; IL-6; 1.
ET NON TER 1 1

FT	NON_TER	I	I	
FT	NON_TER	101	101	
SQ	SEQUENCE	101 AA;	11749 MW;	DIDA362A CRC32:

Query Match	21.5%	Score 320;	DB 11;	Length 101;
Best Local Similarity	40.2%	Pred. No. 1.51e-40;		
Matches	39; Conservative	27; Mismatches	30; Indels	

```
Db      5 NDGCTGTGNWEICLLKITSGLLDYIYLEFVTNNVDNKKDKARVIOSTTKTLISOIFKQ 64
        :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||::
Qy     98 KDCGFQSFGNEETLKVKIITGLLEFFVYLEYLONRF-SSSECARAVOMSTKYLIOLFLOK 156
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Db 65 EVKDPDKIVMPSPSTSKAILIEKLESQKWPRTKTIEL 101
      : | | | | | : | | | | | : | | | | | : |
Qy 157 KAKNLDIAITPDPTTNASLLTKLOAONOWLEDMPTHL 193

```

RESULT 10
ID O40918
PRELIMINARY:
PRT: 204 AA.

040516;
AC DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JAN-1998 (TREMBLrel. 08, Last annotation update)
DE ORF K2.

OC Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.

RN	[1]	SEQUENCE FROM N.A.
RP		

RX MEDLINE: 97138401.
 RA NEIPEL F., ALBRECHT J.C., ENSER A., HUANG Y.Q., LI J.J.,
 RA FRIEDMAN-KIEN A.E., FLECKENSTEIN B.;
 RA "Human herpesvirus 8 encodes a homolog of interleukin-6." *J. Virol.* 71:839-842(1997).
 RT
 RL

RN	[2]	RP
		SEQUENCE FROM N.A.

RX MEDLINE; 97296220.
RA NEIPEL F., ALBRECHT J.C., FLECKENSTEIN B.;

"Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus human herpesvirus 8: determinants of its pathogenicity?"
J. Virol. 71:4187-4192(1997).

DR EMBL; U93872; AAB62676.
DR PFAM; PF00489; IL-6; 1.
SO SEQUENCE 304 AA; 32A

SEQUENCE 204 AA; 23408 MW; 54BB/A6F CRC32;

	Query Match	17.2%	Score 256;	DB 14;	Length 204;
	Best Local Similarity	27.7%;	Pred. No. 6.83e-28;		
	Matches	39;	Conservative	38;	Mismatches 64; Indels 0; Gaps 0;
Db	51	RDLVRTGICKGILEPAAIPHKLKLPALINDPDHGLLGIFNETSLCKLADGGFFFFEVLRFK	110		
		:: :			
Qy	69	KETCNKNMCESSPEALAENLNLPKMAEKDGCFCQSGFNEETCLVKIITGLLEFEVYLEY	128		
		:: :			
Db	111	LTTEFGFSVINVDVMYELLTTLGDIOEELNKLTHTHYSPPKDFRDLGLRLQLSKYVVRRH	170		
		: :			
Qy	129	LQNFESESEQARAVOMSTKVLFQFLQKKAKNLDAITTPDPPTNASLLTKLQAQNWLED	188		
		: :			
Db	171	FASFYVLGAMEKFAGQAVRVL	191		
		:: :			
Qy	189	MPHLILRSILKEFLORSRAL	209		

RESULT 11
ID Q98823
PRELIMINARY;
PRT: 204 AA.

AC	Q98823;			
DT	01-FEB-1997	(TREMBLrel. 02, Created)		
DD	01-FEB-1997	(TREMBLrel. 02, Last sequence update)		
DE	01-NOV-1998	(TREMBLrel. 08, Last annotation update)		
DE		INTERLEUKIN-6 HOMOLOG (FRAGMENT).		

DE
GN
OS
OS
OS
OS
OC
OC
OC

MILKREIN V BOROOG (FRAGMENT).
VIL-6.
Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8),
and Kaposi's sarcoma-associated herpesvirus (KSHV)
(Human herpesvirus 8).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.

[1]
RN SEQUENCE FROM N.A.
EP NEIPEL F., ALBRECHT J.C., ENSSER A., HUANG Y.Q., LI J.J.,
RA FRIEDMAN-KIDEN A.E., FLECKENSTEIN B.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

RN [2]
RP SEQUENCE FROM N.A.

RA NICHOLAS J., RUVOLO V.R., BURNS W.H., SANDFORD G., WAN X., CIUFO D.,
RA HENDRICKSON S., GUO H.G., HAYWARD G.S., REITZ M.S.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases

RN	[3]	SEQUENCE FROM N.A.
RP		
RV		

RA MEDLINE; 97094384.
RX MOORE P.S., BASHOFF C., WEISS R.A., CHANG Y.:
RT "Molecular mimicry of human cytokine and cytokine response pathway
RT genes by KSHV.";
RL Science 274:1739-1744(1996).

RN	[4]	SEQUENCE FROM N.A.
RP		

RX MEDLINE; 97121480.
 RA RUSSO J.J., BOHENZKY R.A., CHIEN M.C., CHEN J., YAN M., MADDALENA D.,
 RA PARRY J.P., PERUZZI D., EDELMAN I.S., CHANG Y., MOORE P.S.;
 RT "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
 (HHV8).";

Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
[5]

RP SEQUENCE FROM N.A.
RA RUSSO J.J., BOHENZKY R.A., CHIEN M.C., CHEN J., YAN M., MADDALENA D.,
RA PARRY J.P., PERUZZI D., EDELMAN I.S., CHANG Y., MOORE P.S.;
RL Submitted (OCT-1996) to the EMBL/Genbank/DDBJ databases.
[6]

RP SEQUENCE FROM N.A.
RA RUSSO J.J., BOHENZKY R.A., CHEN M.C., CHEN J., YAN M., MADDALENA D.,
RA PARRY J.P., PERUZZI D., EDELMAN I.S., CHANG Y., MOORE P.S.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [7]

RC SPECIES=KSHV;
RP SEQUENCE FROM N.A.

RA SUN R., LIN S.-F., MILLER G.?
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U73655; AAB18244.1; -.
DR EMBL; U67774; AAB61701.1; -.

[illegible]

QY 72 CKNSNCESSPALAENNLNPKMAEKDGCFSQSGFNEETCLVKIITGLLEFEVLEYLQN 131
Db 124 LDDAPGDADAAAGSANTVVLVSALDSLIEELPVNNKIGGAESNEKTVRALGGQSPRDVV 183
QY 132 REF-SS-EQARAVOMSTKVLIQFLQKKAKNLDAITT-PDPTTNASLLTKLQAQNWLED 188
Db 184 LSAFRILEYQLMFLRDGRRAIAMM 207
QY 189 MPHTLILRSKREFLQSLRALRQM 212

RESULT 15
ID P97712 PRELIMINARY; PRT; 214 AA.
AC P97712;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE GRANULOCYTE COLONY STIMULATING FACTOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97074656.
RA HAN S.W., RAMESH N., OSBORNE W.R.A.;
RT "Cloning and expression of the cDNA encoding rat granulocyte colony-
stimulating factor";
RL Gene 175:101-104(1996).
DR EMBL; U37101; AAC52915.1; -.
DR HSSP; P09919; IRHG.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR PFAM; PF00489; IL-6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
SQ SEQUENCE 214 AA; 23659 MW; F2592D0C CRC32;

Query Match 7.6%; Score 113; DB 11; Length 214;
Best Local Similarity 21.0%; Pred. No. 9.18e-03;
Matches 33; Conservative 40; Mismatches 79; Indels 5; Gaps 5;
Db 47 QVRKIQARNTLEQLCATYKLCHPPELVLFHSHLIGIPK-ASLSSCSQALQQTCLSQL 105
QY 56 QIRYILDGIALRKETCNKSNCESSPEALAEENNLNPKMAEKDGCFSQSGFNEETCLVKI 115
Db 106 HSGFLYQGLLQALAG-I-SSE-LAPTIDMLHLDVDNFATTIWOQMESLGA-PTVPTQ 161
QY 116 ITGLLEFEVLEYLQNRFESESEQARAVOMSTKVLIQFLQKKAKNLDAITTPDPTTNASL 175
Db 162 STMPIFTSAFORRAGGLVLTYSLOSFLETAHHL 198
QY 176 LTKLQAQNWLEDMPHTLILRSKREFLQSLRALRQM 212

Search completed: Thu Aug 10 16:30:56 2000
Job time : 118 secs.

W P S R L
(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Aug 10 16:28:03 2000; MasPar time 8.51 Seconds
Tabular output not generated. 772.408 Million cell updates/sec

Title: >US-09-142-471-5
Description: (1-212) from US09142471.pep
Perfect Score: 1485
Sequence: 1 MNSFSTSAFGPVAFSLGELL.....LILRSKLEFLQSLRALRQM 212

Scoring table: PAM 150
Gap 11

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot38
1:swissprot

Statistics: Mean 47.239; Variance 84.998; scale 0.556

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1446	97.4	212	1 IL6_HUMAN	INTERLEUKIN-6 PRECURSOR	5.60e-297
2	1410	94.9	212	1 IL6_MACMU	INTERLEUKIN-6 PRECURSOR	1.45e-288
3	1403	94.5	212	1 IL6_CERTO	INTERLEUKIN-6 PRECURSOR	6.25e-287
4	1402	94.4	212	1 IL6_MACFA	INTERLEUKIN-6 PRECURSOR	1.07e-286
5	953	64.2	212	1 IL6_PIG	INTERLEUKIN-6 PRECURSOR	1.50e-182
6	940	63.3	209	1 IL6_PHOVI	INTERLEUKIN-6 PRECURSOR	1.46e-179
7	939	63.2	208	1 IL6_HORSE	INTERLEUKIN-6 PRECURSOR	2.47e-179
8	891	60.0	205	1 IL6_ORCOR	INTERLEUKIN-6 PRECURSOR	2.54e-168
9	891	60.0	208	1 IL6_FELCA	INTERLEUKIN-6 PRECURSOR	2.54e-168
10	875	58.9	207	1 IL6_CANFA	INTERLEUKIN-6 PRECURSOR	1.17e-164
11	807	54.3	208	1 IL6_CAPHI	INTERLEUKIN-6 PRECURSOR	3.94e-149
12	804	54.1	208	1 IL6_SHEEP	INTERLEUKIN-6 PRECURSOR	1.90e-148
13	804	54.1	208	1 IL6_BOVIN	INTERLEUKIN-6 PRECURSOR	1.90e-148
14	710	47.8	207	1 IL6_MARMO	INTERLEUKIN-6 PRECURSOR	4.04e-127
15	650	43.8	211	1 IL6_MOUSE	INTERLEUKIN-6 PRECURSOR	1.33e-113
16	642	43.2	211	1 IL6_RAT	INTERLEUKIN-6 PRECURSOR	8.29e-112
17	490	33.0	125	1 IL6_MUSVI	INTERLEUKIN-6 (IL-6) (4.50e-78
18	166	11.2	201	1 MGF_CHICK	MYELOMONOCYTIC GROWTH	1.20e-11
19	126	8.5	194	1 CSF3_FELCA	GRANULOCYTE COLONY-STI	5.78e-05
20	116	7.8	175	1 CSF3_CANFA	GRANULOCYTE COLONY-STI	1.94e-03
21	108	7.3	208	1 CSF3_MOUSE	GRANULOCYTE COLONY-STI	2.85e-02
22	109	7.3	1102	1 MYSC_CHICK	MYOSIN HEAVY CHAIN, CA	2.05e-02
23	103	6.9	454	1 MSRE_RABIT	MACROPHAGE SCAVENGER R	1.43e-01

24	103	6.9	2209	1 Y166_HUMAN	HYPOTHETICAL PROTEIN K	1.43e-01
25	99	6.7	195	1 CSF3_PIG	GRANULOCYTE COLONY-STI	5.01e-01
26	100	6.7	456	1 PTSB_KLEPN	PTS SYSTEM, SUCROSE-SP	3.68e-01
27	99	6.7	759	1 RRP3_IARUD	RNA-DIRECTED RNA POLYM	5.01e-01
28	99	6.7	759	1 RRP3_IAGU2	RNA-DIRECTED RNA POLYM	5.01e-01
29	99	6.7	759	1 RRP3_IAGUA	RNA-DIRECTED RNA POLYM	5.01e-01
30	99	6.7	1427	1 RRP3_HUMAN	RESTIN (CYTOPLASMIC LI	5.01e-01
31	98	6.6	199	1 IL11_HUMAN	INTERLEUKIN-11 PRECURS	6.82e-01
32	98	6.6	241	1 RRP3_HRSV1	RNA POLYMERASE ALPHA S	6.82e-01
33	98	6.6	259	1 PP26_BRUAB	26 KDA PERIPLASMIC IMM	6.82e-01
34	97	6.5	341	1 AFP1_HUMAN	ARFAPTIN 1	9.24e-01
35	96	6.5	541	1 PTN5_MOUSE	PROTEIN-TYROSINE PHOSP	1.25e+00
36	96	6.5	692	1 FLHA_YEREN	FLAGELLAR BIOSYNTHESIS	1.25e+00
37	96	6.5	2768	1 THYG_HUMAN	THYOGLOBULIN PRECURSO	1.25e+00
38	94	6.3	174	1 CSF3_SHEEP	GRANULOCYTE COLONY-STI	2.27e+00
39	94	6.3	232	1 TONB_CAMCO	TONB PROTEIN	2.27e+00
40	94	6.3	241	1 RRP3_HRSV	RNA POLYMERASE ALPHA S	2.27e+00
41	94	6.3	241	1 RRP3_HRSVL	RNA POLYMERASE ALPHA S	2.27e+00
42	94	6.3	759	1 RRP3_TAFPW	RNA-DIRECTED RNA POLYM	2.27e+00
43	94	6.3	759	1 RRP3_TALE2	RNA-DIRECTED RNA POLYM	2.27e+00
44	93	6.3	759	1 RRP3_IASE2	RNA-DIRECTED RNA POLYM	3.05e+00
45	94	6.3	1764	1 YKB4_YEAST	HYPOTHETICAL 203.3 KDA	2.27e+00

ALIGNMENTS

RESULT 1	IL6_HUMAN	STANDARD;	PRT;	212 AA.
AC	P05231;			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2)			
DE	(INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR).			
GN	IL6 OR IFNB2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE; 87065033.			
RA	Hirano T., Yasukawa K., Harada H., Taga T., Watanabe Y., Matsuda T.,			
RA	Kashiwamura S.-I., Nakajima K., Koyama K., Iwamatsu A., Tsunawasa S.,			
RA	Sakiguchi F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.;			
RT	"Complementary DNA for a novel human interleukin (BSF-2) that induces			
RT	B lymphocytes to produce immunoglobulin.";			
RL	Nature 324:73-76(1986).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 88082664.			
RA	Yasukawa K., Hirano T., Watanabe Y., Muratani K., Matsuda T.,			
RA	Nakai S., Kishimoto T.;			
RT	"Structure and expression of human B cell stimulatory factor-2			
RT	(BSF-2/IL-6) gene.";			
RL	EMBO J. 6:2939-2945(1987).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 87067433.			
RA	May L.T., Helfgott D.C., Sehgal P.B.;			
RT	"Anti-beta-interferon antibodies inhibit the increased expression of			
RT	HUA-87 mRNA in tumor necrosis factor-treated human fibroblasts:			
RT	structural studies of the beta 2 interferon involved.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 87053818.			
RA	Zilberstein A., Ruggieri R., Korn J.H., Revel M.;			
RT	"Structure and expression of cDNA and genes for human			
RT	interferon-beta-2, a distinct species inducible by growth-stimulatory			
RT	cytokines.";			
RL	EMBO J. 5:2529-2537(1986).			
RN	[5]			
RP	SEQUENCE FROM N.A.			

RX MEDLINE; 88088768.
RA Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
RA Aarden L.A.,
RT "Molecular cloning and expression of hybridoma growth factor in
RT Escherichia coli";
RL J. Immunol. 139:4116-4121(1987).
RN [16]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89391958.
RA Tonouchi N., Miwa K., Karasuyama H., Matsui H.;
RT "Deletion of 3' untranslated region of human BSF-2 mRNA causes
RT stabilization of the mRNA and high-level expression in mouse NIH3T3
RT cells";
RL Biochem. Biophys. Res. Commun. 163:1056-1062(1989).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89193317.
RA Wong G., Witke-Giannotti J., Hewick R., Clark S., Ogawa M.;
RT "Interleukin 6: Identification as a hematopoietic colony-stimulating
RT factor";
RL Behring Inst. Mitt. 83:40-47(1988).
RN [9]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93178270.
RA Chen Q.Y.;
RT "Stable and efficient expression of human interleukin-6 cDNA in
RT mammalian cells after gene transfer";
RL Chung-Hua Chung Liu Tsa Chih 14:340-344(1992).
RN [10]
RP SEQUENCE OF 30-63.
RX MEDLINE; 88154445.
RA van Damme J., van Beunnen J., Decock B., van Snick J., de Ley M.,
RA Billiau A.;
RT "Separation and comparison of two monokines with
RT lymphocyte-activating factor activity: IL-1 beta and hybridoma growth
RT factor (HGF). Identification of leukocyte-derived HGF as IL-6";
RL J. Immunol. 140:1534-1541(1988).
RN [11]
RP SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING 1ST DISULFIDE BOND.
RX MEDLINE; 95154344.
RA Breton J., la Fiura A., Bertolero F., Orsini G., Valsasina B.,
RA Ziliotto R., de Filippis V., Polverino de Laureto P., Fontana A.;
RT "Structure, stability and biological properties of a N-terminally
RT truncated form of recombinant human interleukin-6 containing a single
RT disulfide bond";
RL Eur. J. Biochem. 227:573-581(1995).
RN [12]
RP DISULFIDE BONDS.
RX MEDLINE; 89286115.
RA Clogston C.L., Boone T.C., Crandall B.C., Mendiaz E.A., Lu H.S.;
RT "Disulfide structures of human interleukin-6 are similar to those of
RT human granulocyte colony stimulating factor";
RL Arch. Biochem. Biophys. 272:144-151(1989).
RN [13]
RP MUTAGENESIS.
RX MEDLINE; 91243808.
RA Luetticken C., Kruettgen A., Moeller C., Heinrich P.C., Rose-John S.;
RT "Evidence for the importance of a positive charge and an
RT alpha-helical structure of the C-terminus for biological activity of
RT human IL-6";
RL FEBS Lett. 282:265-267(1991).
RN [14]
RP STRUCTURE BY NMR.
RX MEDLINE; 96134845.

RA Nishimura C., Watanabe A., Gouda H., Shimada I., Arata Y.;
RT "Folding topologies of human interleukin-6 and its mutants as studied
RT by NMR spectroscopy";
RL Biochemistry 35:273-281(1996).
RN [15]
RP STRUCTURE BY NMR.
RX MEDLINE; 97303053.
RA Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
RA Cumming D.A.;
RT "Solution structure of recombinant human interleukin-6";
RL J. Mol. Biol. 268:468-481(1997).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE; 97224126.
RA Somers W., Stahl M., Seehra J.S.;
RT "1.9-A crystal structure of interleukin 6: implications for a novel
RT mode of receptor dimerization and signaling";
RL EMBO J. 16:989-997(1997).
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC -----
DR EMBL; X04430; CAA28026.1; -
DR EMBL; M14584; AAA52728.1; -
DR EMBL; X04602; CAA28268.1; -
DR EMBL; Y00081; CAA68278.1; -
DR EMBL; M18403; AAA52729.1; -
DR EMBL; M29150; AAA59154.1; -
DR EMBL; X04402; CAA27990.1; -
DR EMBL; X04403; CAA27991.1; -
DR EMBL; M54894; AAC41704.1; -
DR EMBL; S56892; AAD13886.1; -
DR EMBL; A09363; CAA00839.1; -
DR PIR; A32648; IVHUB2.
DR PIR; A25921; A25921.
DR PDB; 1IL6; 04-FEB-98.
DR PDB; 2IL6; 04-FEB-98.
DR PDB; 1ALU; 03-JUN-98.
DR MIM; 147620; -
DR PFAM; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFPMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal; 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78
FT DISULFID 101 111
FT CARBOHYD 73 73
FT MUTAGEN 173 173 A->V: ALMOST NO LOSS OF ACTIVITY.
FT MUTAGEN 185 185 W->R: NO LOSS OF ACTIVITY.
FT MUTAGEN 204 204 S->P: 13% ACTIVITY.
FT MUTAGEN 210 210 R->K,E,Q,T,A,P: LOSS OF ACTIVITY.
FT MUTAGEN 212 212 M->T,N,S,R: LOSS OF ACTIVITY.
SQ SEQUENCE 212 AA; 23718 MW; 1F1ED1E1B734079 CRC64;

Query Match 97.4%; Score 1446; DB 1; Length 212;
Best Local Similarity 97.6%; Pred. No. 5.60e-297;
Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

DB 1 MNSFTSAFGPVAFSLGLLLVLPAAFPAPVPPGDSKDVAAFPHPROPLTSSEKIDKOIRY 60
|||||

OY 1 MNSFSAFGVAFSLGILLVLPAAFPAPVPPGDSKDVAAAPHQPLTSSERIDKHRYI 60
 Db 61 LDGIALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFOGSGNEETCLVKIITGLL 120
 OY 61 LDGIALRKETCNKSNMCESSPEALAENNLNLPKMAEKDGCFOGSGNEETCLVKIITGLL 120
 Db 121 EFVYLEYLQNRFFESSEBQARAVQMSKVLQFLOKKAKNLDAITTPDPTTNASLLTKLQ 180
 OY 121 EFVYLEYLQNRFFESSEBQARAVQMSKVLQFLOKKAKNLDAITTPDPTTNASLLTKLQ 180
 Db 181 AQONWLODMTHLLRSFKFELQSLRALROM 212
 OY 181 AQONWLEDMPTHLLRSKKEFLQSLRALROM 212

RESULT 2
 ID IL6_MACMU STANDARD; PRT; 212 AA.
 AC P51494;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RAC 2;
 RX MEDLINE; 96003435.
 RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and
 nonhuman primates.";
 RL J. Immunol. 155:3946-3954(1995).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; L26028; AAA99978.1; -
 DR HSSP; P05231; 1ALU.
 DR PFAM; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GSGFMGF.
 DR PRINTS; PR00434; INTERLEUKIN_6.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29 BY SIMILARITY.
 FT CHAIN 30 212 INTERLEUKIN-6.
 FT DISULFID 72 78 POTENTIAL.
 FT DISULFID 101 111 POTENTIAL.
 FT CARBOHYD 73 73 POTENTIAL.
 FT CARBOHYD 172 172 POTENTIAL.
 SQ SEQUENCE 212 AA; 23728 MW; 4130DFE0CF0BCCAD CRC64;

Query Match 94.9%; Score 1410; DB 1; Length 212;
 Best Local Similarity 93.9%; Pred. No. 1.45e-288;
 Matches 199; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Db 1 MNSFSAFGVAFSLGILLVLPAAFPAPVPPGDSKDVAAAPHQPLTSSERIDKHRYI 60
 OY 1 MNSFSAFGVAFSLGILLVLPAAFPAPVPPGDSKDVAAAPHQPLTSSERIDKHRYI 60

Db 61 LDGIALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFOGSGNEETCLVKIITGLL 120
 OY 61 LDGIALRKETCNKSNMCESSPEALAENNLNLPKMAEKDGCFOGSGNEETCLVKIITGLL 120
 Db 121 EFVYLEYLQNRFFESSEBQARAVQMSKVLQFLOKKAKNLDAITTPDPTTNASLLTKLQ 180
 OY 121 EFVYLEYLQNRFFESSEBQARAVQMSKVLQFLOKKAKNLDAITTPDPTTNASLLTKLQ 180
 Db 181 AQONWLODMTHLLRSFKFELQSLRALROM 212
 OY 181 AQONWLEDMPTHLLRSKKEFLQSLRALROM 212

RESULT 3
 ID IL6_CERTO STANDARD; PRT; 212 AA.
 AC P46550;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Carcocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Cercocebus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FUJ;
 RX MEDLINE; 96003435.
 RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and
 nonhuman primates.";
 RL J. Immunol. 155:3946-3954(1995).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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 CC
 CC EMBL; L26032; AAA99972.1; -
 DR HSSP; P05231; 1ALU.
 DR PFAM; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GSGFMGF.
 DR PRINTS; PR00434; INTERLEUKIN_6.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29 BY SIMILARITY.
 FT CHAIN 30 212 INTERLEUKIN-6.
 FT DISULFID 72 78 POTENTIAL.
 FT DISULFID 101 111 POTENTIAL.
 FT CARBOHYD 73 73 POTENTIAL.
 FT CARBOHYD 172 172 POTENTIAL.
 SQ SEQUENCE 212 AA; 23668 MW; C73C035226B44B9F CRC64;

Query Match 94.5%; Score 1403; DB 1; Length 212;
 Best Local Similarity 93.4%; Pred. No. 6.25e-287;
 Matches 198; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Db 1 MNSFSAFGVAFSLGILLVLPAAFPAPVPPGDSKDVAAAPHQPLTSSERIDKHRYI 60
 OY 1 MNSFSAFGVAFSLGILLVLPAAFPAPVPPGDSKDVAAAPHQPLTSSERIDKHRYI 60
 Db 61 LDGIALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFOGSGNEETCLVKIITGLL 120

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QY 61 LDGIALRKETCNKSNMCESSPEALAEANNLNPMAEKDGCQFSGFNEETCLVKIITGLL 120
Db 121 EFVYLEYLQNRFSSEEQARAVOMSTKVLIQLOKKAKNLDAITTPPTNASLLTKLQ 180
QY 121 EFVYLEYLQNRFSSEEQARAVOMSTKVLIQLOKKAKNLDAITTPPTNASLLTKLQ 180
Db 181 AQONWLODMTHILRSFKFLOSLRALROM 212
QY 181 AQONWLEDMPTHLILRSKFLQSLRALROM 212

RESULT 4
ID IL6_MACFA STANDARD; PRT; 212 AA.
AC P79341;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Macaca.
RN [1]
RP SEQUENCE FROM N.A.
RA Tatsumi M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
CC EMBL; AB000554; BAA19148.1; -.
CC HSSP; P05231; 2IL6.
CC PFAM; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC PROSITE; PR00434; INTERLEUKIN_6.
CC CYTOKINE; Glycoprotein; Growth factor; Signal.
CC SIGNAL 1 29 BY SIMILARITY.
CC CHAIN 30 212 INTERLEUKIN-6.
CC DISULFID 72 78 POTENTIAL.
CC FT CARBOHYD 73 73 POTENTIAL.
CC FT CARBOHYD 172 172 POTENTIAL.
CC SEQUENCE 212 AA; 23654 MW; CF8173FCBF080389 CRC64;

Query Match 94.4%; Score 1402; DB 1; Length 212;
Best Local Similarity 94.3%; Pred. No. 1.07e-286;
Matches 200; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Db 1 MNSVTSAGFPVAFSLGILLVLPAAFPAPVPGEDSKDVAAPHQPLTSSERIDKHIRYI 60
QY 1 MNSFSTAGFPVAFSLGILLVLPAAFPAPVPGEDSKDVAAPHQPLTSSERIDKHIRYI 60
Db 61 LDGIALRKETCNKSNMCESSPEALAEANNLNPMAEKDGCQFSGFNEETCLVKIITGLL 120
QY 61 LDGIALRKETCNKSNMCESSPEALAEANNLNPMAEKDGCQFSGFNEETCLVKIITGLL 120
Db 121 EFVYLEYLQNRFSSEEQARAVOMSTKVLIQLOKKAKNLDAITTPPTNASLLTKLQ 180
QY 121 EFVYLEYLQNRFSSEEQARAVOMSTKVLIQLOKKAKNLDAITTPPTNASLLTKLQ 180

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Db 181 AQONWLODMTHILRSFKFLOSLRALROM 212
QY 181 AQONWLEDMPTHLILRSKFLQSLRALROM 212

RESULT 5
ID IL6_PIG STANDARD; PRT; 212 AA.
AC P26893;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
RA Richards C.; Saklatvala J.;
RT "Molecular cloning and sequence of porcine interleukin 6 cDNA and
RT expression of mRNA in synovial fibroblasts in vitro.";
RL Cytokine 3:269-276(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Mathialagan N.;
RL "Expression of Interleukin-6 in porcine, ovine, and bovine
RL preimplantation conceptuses.";
RL Mol. Reprod. Dev. 32:324-330(1992).
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M86722; AAC37333.1; -.
CC EMBL; M80258; AAC27127.1; -.
CC HSSP; P05231; 1ALU.
CC PFAM; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC PROSITE; PR00434; INTERLEUKIN_6.
CC CYTOKINE; Glycoprotein; Growth factor; Signal.
CC SIGNAL 1 29 BY SIMILARITY.
CC CHAIN 30 212 INTERLEUKIN-6.
CC DISULFID 72 78 BY SIMILARITY.
CC FT CARBOHYD 73 73 BY SIMILARITY.
CC FT CARBOHYD 172 172 BY SIMILARITY.
CC FT CONFLICT 30 30 G -> E (IN REF. 2).
CC SEQUENCE 212 AA; 23880 MW; EF100ED030B6FDD0 CRC64;

Query Match 64.2%; Score 953; DB 1; Length 212;
Best Local Similarity 61.3%; Pred. No. 1.50e-182;
Matches 130; Conservative 42; Mismatches 40; Indels 0; Gaps 0;

Db 1 MNSLSTAFSPVAFSLGILLVLPAAFPAPVPGEDSKDVAAPHQPLTSSERIDKHIRYI 60
QY 1 MNSFSTAGFPVAFSLGILLVLPAAFPAPVPGEDSKDVAAPHQPLTSSERIDKHIRYI 60
Db 61 LGKISARKECKEYKCEKSNKEVLAENNLNLPMAEKDGCQFSGFNEETCLMRITGLV 120
QY 61 LGKISARKECKEYKCEKSNKEVLAENNLNLPMAEKDGCQFSGFNEETCLMRITGLV 120
Db 121 EFQIYLDYLOKEYESKNGVNEAVQISTKALIQTLROKGNPKDKATPPTNAGLLDKLQ 180

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Db 183 LKHTTIIILRSLEDFLQFSLRAVRIM 209

QY 61 LOGISALRKTCKNSMCESSPEALANNLNPMAEKDCQSGFNEETCLVKITGLL 120
 Db 118 EFOIYLEYLQNEFKGKBNKIMQJSTKVLVOILMOKKNPE-VTTPOPTAKSLAKLH 176
 QY 121 EFEVLEYLQNEFSEGEARQVSTKVLIQFQKKAKNLDATTPDPTTNASLTQLQ 180
 Db 177 SONEWLKNTTTHILRSLEDFLQFSRAVRIM 208
 QY 181 AQOWLEDMPTHLILRSLEFLQFSRALRQM 212

RESULT 8
 ID IL6_ORCOR STANDARD; PRT; 205 AA.
 AC Q28747;
 DT 15-FEB-2000 (Rel. 39, Created)
 DT 15-FEB-2000 (Rel. 39, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
 GN IL6.
 OS Orcinus orca (Killer whale).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
 OC Orcinus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96163018.
 RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
 RA Stott J.L., Ferrick D.A.;
 RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
 RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
 RT Southern sea otter (Enhydra lutris nereis).";
 RL Immunogenetics 43:190-195(1996).
 CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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 EMBL; L48803; AB01429.1; -;
 DR HSSP; P05231; IALU.
 DR PFAM; PF00489; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR CYTOKINE; Glycoprotein; Growth factor; Signal.
 KW NON_TER 1 1
 FT SIGNAL <1 21 BY SIMILARITY.
 FT CHAIN 22 205 INTERLEUKIN-6.
 FT DISULFID 64 70 BY SIMILARITY.
 FT DISULFID 93 103 BY SIMILARITY.
 FT CARBOHYD 164 164 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 205 AA; 23266 MW; 6308F34457960832 CRC64;

Query Match 60.0%; Score 891; DB 1; Length 205;
 Best Local Similarity 61.8%; Pred. No. 2.54e-168;
 Matches 123; Conservative 38; Mismatches 37; Indels 1; Gaps 1;

Db 5 AFSGLLLVYATAPPTGPGIPEGDKDFTSDRLYLSPDKTEALIKYLKISAMKEMC 64
 QY 13 AFSGLLLVLPAPAPVPPGDSKVAAPHROPLTSSERIDKQIRYILDGIALRKTC 72
 Db 65 EKYDKNSKEALANNLNPMAEKDCQSGFNEETCLVKITGLLEFVLEYLQNR 124
 QY 73 NKSNCWESSPEALANNLNPMAEKDCQSGFNEETCLVKITGLLEFVLEYLQNR 132

Db 125 YEGDKEATEAVQISSKALAQILROKVKNPDEVTPDPTTNASLMNLOSQNDWMKNTKI 184
 QY 133 FESSEQARAVQSTKVLIQFQKKAKNLDATTPDPTTNASLTQLQAOQ-WLEDMPT 191
 Db 185 ILILRSLEFLQFSRAIR 203
 QY 192 HLILRSLEFLQFSRALR 210

RESULT 9
 ID IL6_FELCA STANDARD; PRT; 208 AA.
 AC P41683;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Carnivora; Fissipedia; Felidae; Felis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94162386.
 RA Ohashi T., Matsumoto Y., Watari T., Goitsuka R., Tsujimoto H.,
 RA Hasegawa A.;
 RT "Molecular cloning of feline interleukin-6 cDNA";
 RL J. Vet. Med. Sci. 55:941-944(1993).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC TISSUE-LYMPHOCTES;
 CC MEDLINE; 94052249.
 RA Bradley W.G., Gibbs C., Kraus L., Good R.A., Day N.K.;
 RT "Molecular cloning and characterization of a cDNA encoding feline
 RT interleukin-6";
 RL Proc. Soc. Exp. Biol. Med. 204:301-305(1993).
 CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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 EMBL; L16914; AAA16620.1; -;
 DR EMBL; D13227; BAA02507.1; -;
 DR HSSP; P05231; 2IL6.
 DR PFAM; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN_6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 208 INTERLEUKIN-6.
 FT DISULFID 68 74 BY SIMILARITY.
 FT DISULFID 97 107 BY SIMILARITY.
 FT CONFLICT 2 2 T -> N (IN REF. 2).
 FT CONFLICT 45 45 S -> P (IN REF. 2).
 FT CONFLICT 133 133 E -> K (IN REF. 2).
 FT CONFLICT 173 187 AKLQSQEWLRHTTI -> LSCSHRRVAAHNN (IN
 FT REF. 2).
 FT CONFLICT 200 201 FS -> LR (IN REF. 2).
 SQ SEQUENCE 208 AA; 23401 MW; 93B4456B2989CA4C CRC64;

Query Match 60.0%; Score 891; DB 1; Length 208;
 Best Local Similarity 57.5%; Pred. No. 2.54e-168;

[illegible]

Query Match	54.1%	Score 804;	DB 1;	Length 208;
Best Local Similarity	52.9%	Pred. No. 1.90e-148;		

Search completed: Thu Aug 10 16:28:41 2000
Job time : 38 secs.

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RT sequence and relation to human interleukin-6.";  
RL Eur. J. Biochem. 176:187-197(1988).  
RN [8]  
RP SEQUENCE OF 66-75; 78-84 AND 128-148.  
RX MEDLINE: 90147691.  
RA Jahnen W., Ward L.D., Reid G.E., Moritz R.L., Simpson R.J.;  
RT "Internal amino acid sequencing of proteins by in situ cyanogen  
bromide cleavage in polyacrylamide gels.";  
RL Biochem. Biophys. Res. Commun. 166:139-145(1990).  
RN [9]  
RP SEQUENCE OF 25-45.  
RX MEDLINE: 87092311.  
RA van Snick J., Cayphas S., Vink A., Uyttenhove C., Coulie P.G.,  
Rubira M.R., Simpson R.J.;  
RT "Purification and NH2-terminal amino acid sequence of a  
T-cell-derived lymphokine with growth factor activity for B-cell  
hybridomas.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:9679-9683(1986).  
CC -I- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL  
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND  
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN  
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.  
CC -I- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL: X06203; CAA29560.1; -  
DR EMBL: M20572; AAA39302.1; -  
DR EMBL: X51457; CAA35824.1; -  
DR EMBL: J03783; AAA39301.1; -  
DR EMBL: X54542; CAA38411.1; -  
DR EMBL: M24221; AAA68814.1; -  
DR PIR: A30531; ICMS6.  
DR HSP: P05231; IALU.  
DR MGD; MGI:96559; IL6.  
DR PFAM: PF00489; IL6.1.  
DR PRINTS; PR00433; IL6GCSFMGF.  
DR PRINTS; PR00434; INTERLEUKIN6.  
DR PROSITE; PS00254; INTERLEUKIN_6; 1.  
KW Cytokine; Growth factor; Glycoprotein; Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 211 INTERLEUKIN-6.  
FT DISULFD 70 76 BY SIMILARITY.  
FT DISULFD 99 109 BY SIMILARITY.  
FT SEQUENCE 211 AA; 24384 MW; BBB47DDA9E86787A CRC64;  
  
Query Match 43.8%; Score 650; DB 1; Length 211;  
Best Local Similarity 41.8%; Pred.No. 1.33e-113;  
Matches 89; Conservative 55; Mismatches 64; Indels 5; Gaps 5;  
  
Db 1 MKFLSARDHPVAF-LGLMLVTTTAPFTSQVRGDFED-TTPNR-PVYTTQVQGLITH 57  
QY 1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAP-VPPGEDSKDVAAPHQPLTSSERIDKQIRY 59  
  
Db 58 VLWEIVEMRKELCNGNSDCMNDALANNKLPFIQRNDGCGYQGYNQEIICLLKISSGL 117  
QY 60 ILDGISALRKETCKNSKNCSPEALAEANNLNLPRMAEKDGCFCQSGFNEETCLVKIITGL 119  
  
Db 118 LEYHSYLEYMKNNKDKRKLQRTDTLHIFNEQVKDLHKIVLPTPISNALLTDK 177  
QY 120 LEFEVYLEYLNRF-ESSEEQARQVMSKVLQFLQKAKNLDAITTPDTTNASLITK 178  
  
Db 178 LESQKWLRTKIQFILKSLSEFLKVLTRSTQ 210  
QY 179 LQAQNWLEDMPHTHLILRSKFLQSLRALRQ 211
```

M P S R H

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Aug 10 16:26:52 2000; MasPar time 13.10 Seconds
Tabular output not generated. 763.396 Million cell updates/sec

Title: >US-09-142-471-5
Description: (1-212) from US09142471.pep
Perfect Score: 1485
Sequence: 1 MNSFSTSAFGPVAFSLGILL.....LILSLKEFLQSRALRQM 212
Scoring table: PAM 150
Gap 11
Searched: 142080 seqs, 47172406 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: pir64
1:pir1 2:pir2 3:pir3 4:pir4
Statistics: Mean 46.233; Variance 94.667; scale 0.488

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1446	97.4	212	1	interleukin-6 precurs	2.92e-261
2	953	64.2	212	2	prointerleukin 6 - pi	1.35e-160
3	953	64.2	212	2	interleukin 6 - pig	1.35e-160
4	941	63.4	208	2	interleukin-6 precurs	3.60e-158
5	804	54.1	208	1	interleukin-6 precurs	1.39e-130
6	801	53.9	207	2	interleukin 6 - cat	5.54e-130
7	796	53.6	208	1	interleukin-6 - sheep	5.57e-129
8	650	43.8	211	1	interleukin-6 precurs	6.59e-100
9	642	43.2	211	2	interleukin-6 precurs	2.51e-98
10	166	11.2	201	2	myelomonocytic growth	6.08e-10
11	126	8.5	194	2	granulocyte colony-st	5.43e-04
12	119	8.0	656	2	hypothetical protein	4.97e-03
13	113	7.6	214	2	granulocyte colony-st	3.14e-02
14	108	7.3	208	2	granulocyte colony-st	1.40e-01
15	109	7.3	287	2	syntaxin homolog T2H3	1.04e-01
16	109	7.3	321	2	syntaxin homolog T10M	1.04e-01
17	109	7.3	1039	2	myosin heavy chain -	1.04e-01
18	105	7.1	454	2	macrophage scavenger	3.35e-01
19	104	7.0	204	1	granulocyte colony-st	4.47e-01
20	103	6.9	354	2	macrophage scavenger	5.96e-01
21	103	6.9	454	2	macrophage scavenger	5.96e-01
22	101	6.8	314	2	annexin P35 - maize	1.05e-00
23	101	6.8	815	2	high carbon dioxide r	1.05e+00

ALIGNMENTS

RESULT ENTRY	1	24	100	6.7	298	2	S59541	1.39e+00
IVHUB2		25	100	6.7	456	2	S62331	1.39e+00
Interleukin-6 precursor - human		26	99	6.7	779	2	JH0102	1.84e+00
B-cell differentiation factor; B-cell hybridoma growth factor; B-cell stimulating factor 2 (BSF-2); CTL differentiation factor; IL-6; interferon beta-II-a; megakaryocyte potentiation factor		27	99	6.7	1392	2	A43336	1.84e+00
#formal_name Homo sapiens #common_name man		28	99	6.7	1427	2	S22695	1.84e+00
28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 22-Jun-1999		29	99	6.7	1642	2	T08880	1.84e+00
A32648; A25692; A26966; A33515; A25801; A25921; I52193; I56003; A27601; B27601; A60400; A29085; A61159; A61462; A48419; C48419; B48419; JX0305; S04982		30	98	6.6	199	1	B38285	2.42e+00
A32648		31	98	6.6	241	1	RRN218	2.42e+00
Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishimoto, T.		32	98	6.6	520	2	S35575	2.42e+00
EMBO J. (1987) 6:2939-2945		33	97	6.5	341	2	G02515	3.19e+00
Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) gene.		34	96	6.5	692	2	S54214	3.19e+00
#cross-references MUID:88082664		35	96	6.5	880	2	T02245	3.19e+00
#accession A32648		36	96	6.5	2767	1	UIHU	4.19e+00
##molecule_type DNA		37	95	6.4	303	2	S75557	4.19e+00
##residues 1-212 #label YAS		38	95	6.4	341	2	S40612	5.49e+00
##cross-references GB:Y00081; NID:g29494; PIDN:CAA68278.1; PID:g29495		39	95	6.4	533	2	S33744	5.49e+00
##note the authors translated the codon CAG for residue 130 as Glu		40	95	6.4	3738	2	T05501	5.49e+00
REFERENCE		41	94	6.3	174	2	T10268	7.18e+00
A91051		42	94	6.3	736	2	C69451	7.18e+00
Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.		43	94	6.3	759	2	JN0435	7.18e+00
EMBO J. (1986) 5:2529-2537		44	94	6.3	1764	2	S37827	7.18e+00
Structure and expression of cDNA and genes for human interferon-beta-2, a distinct species inducible by growth-stimulatory cytokines.		45	94	6.3	4869	2	S66572	7.18e+00
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##cross-references GB:X04430; NID:g32673; PIDN:CAA28026.1; PID:g32674								
REFERENCE								
A93387								
Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda, T.; Kashiwamura, S.I.; Nakajima, K.; Koyama, K.; Iwamatsu, A.; Tsunawasa, S.; Sakiyama, F.; Matsui, H.; Takahara, Y.; Taniguchi, T.; Kishimoto, T.								
Nature (1986) 324:73-76								
Complementary DNA for a novel human interleukin (BSF-2) that induces B lymphocytes to produce immunoglobulin.								
#cross-references MUID:87065033								
#accession A26966								

##molecule_type mRNA
##residues 1-212 ##label HIR
##cross-references GB:X04602; NID:g33849; PIDN:CRAA28268.1; PID:g33850
REFERENCE
A33515
#authors Tonouchi, N.; Miwa, K.; Karasuyama, H.; Matsui, H.
#journal Biochem. Biophys. Res. Commun. (1989) 163:1056-1062
#title Deletion of 3' untranslated region of human BSF-2 mRNA causes stabilization of the mRNA and high-level expression in mouse NIH3T3 cells.
#cross-references MUID:89391958
#accession A33515
##molecule_type mRNA
##residues 1-212 ##label TON
##cross-references GB:M29150; NID:g186349; PIDN:AAA59154.1; PID:g307063
REFERENCE
A25801
#authors Haegeman, G.; Content, J.; Volckaert, G.; Derynck, R.; Tavernier, J.; Fiers, W.
#journal Eur. J. Biochem. (1986) 159:625-632
#title Structural analysis of the sequence coding for an inducible 26-kDa protein in human fibroblasts.
#cross-references MUID:87004683
#accession A25801
##molecule_type DNA: mRNA
##residues 1-212 ##label HAE
##cross-references GB:X04403
##experimental_source fibroblast
REFERENCE
A25921
#authors May, L.T.; Helfgott, D.C.; Sehgal, P.B.
#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:8957-8961
#title Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts: structural studies of the beta-2 interferon involved.
#cross-references MUID:87067433
#accession A25921
##molecule_type mRNA
##residues 1-212 ##label MAY
##cross-references GB:M14584; NID:g184628; PIDN:AAA52728.1; PID:g306910
REFERENCE
I52193
#authors Wong, G.G.; Witek-Giannotti, J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.
#journal Behring Inst. Mitt. (1988) 83:40-47
#title Interleukin 6: Identification as a hematopoietic colony-stimulating factor.
#cross-references MUID:89193317
#accession I52193
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-212 ##label WON
##cross-references GB:M54894; NID:g186351; PIDN:AAC41704.1; PID:g186352
REFERENCE
I56003
#authors Brakenhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, L.A.
#journal J. Immunol. (1987) 139:4116-4121
#title Molecular cloning and expression of hybridoma growth factor in *Escherichia coli*.
#cross-references MUID:89088768
#accession I56003
##status translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-212 ##label BRA
##cross-references GB:M18403; NID:g184631; PIDN:AAA52729.1; PID:g306911
REFERENCE
A92816
#authors Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De Ley, M.; Billiau, A.
#journal J. Immunol. (1988) 140:1534-1541
#title Separation and comparison of two monokines with lymphocyte-activating factor activity: IL-1-beta and hybridoma growth factor (HGF). Identification of leukocyte-derived HGF as IL-6.
#cross-references MUID:88154445
#accession A27601
##molecule_type protein

##residues 28-51,'X','53-57,'X','59,'X',61 ##label VAN1
#accession B27601
##molecule_type protein
##residues 30-56,'XX','59-61,'X',63 ##label VA2
REFERENCE
A60400
#authors Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
#journal J. Immunol. (1990) 144:1808-1816
#title The human lung fibroblast cell line, MRC-5, produces multiple factors involved with megakaryocytopoiesis.
#cross-references MUID:90171574
#accession A60400
##molecule_type protein
##residues 30-43 ##label YAM
REFERENCE
A29085
#authors Hirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.; Takatsuki, F.; Shimizu, M.; Murashima, A.; Tsunasawa, S.; Sakiyama, F.; Kishimoto, T.
#journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:228-231
#title Human beta-cell differentiation factor defined by an anti-peptide antibody and its possible role in autoantibody production.
#cross-references MUID:87092370
#accession A29085
##molecule_type protein
##residues 29-42 ##label HIR2
REFERENCE
A61159
#authors Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.; Hara, T.; Ishikawa, H.; Arimura, H.; Konno, K.
#journal Anticancer Res. (1991) 11:961-968
#title Purification and characterization of human fibroblast derived differentiation inducing factor for human monoblastic leukemia cells identical to interleukin-6.
#cross-references MUID:91290785
#accession A61159
##molecule_type protein
##residues 30-42 ##label NOD
##experimental_source fibroblast
REFERENCE
A61462
#authors Ming, J.E.; Cernetti, C.; Steinman, R.M.; Granelli-Piperno, A.
#journal J. Mol. Cell. Immunol. (1989) 4:203-212
#title Interleukin 6 is the principal cytolytic T lymphocyte differentiation factor for thymocytes in human leukocyte conditioned medium.
#cross-references MUID:90121567
#accession A61462
##molecule_type protein
##residues 28-48 ##label MIN
##experimental_source leukocyte-conditioned medium
REFERENCE
A48419
#authors May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriskie, J.B.; Sehgal, P.B.
#journal Cytokine (1991) 3:204-211
#title Marked cell-type-specific differences in glycosylation of human interleukin-6.
#cross-references MUID:91355644
#accession A48419
##molecule_type protein
##residues 30-37,'X',39-40 ##label MAY2
##experimental_source FS-4 fibroblasts
##note sequence extracted from NCBI backbone
##note this 28-30K form contained both N-linked and O-linked carbohydrate; a 25K form containing only N-linked carbohydrate was also found
#accession C48419
##molecule_type protein
##residues 28-40 ##label MAY3
##experimental_source FS-4 fibroblasts
##note sequence extracted from NCBI backbone (NCBIP:63787)
##note this 23-25K form contained O-linked but not N-linked carbohydrate
REFERENCE
JX0305
#authors Orita, T.; Oheda, M.; Hasegawa, M.; Kuboniwa, H.; Esaki, K.;

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#journal      Ochi, N.
#title        J. Biochem. (1994) 115:345-350
#cross-references MUID:94266765
#contents     Polyptide and carbohydrate structure of recombinant human
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#accessions   MUID:94266765
#reference     S04981
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Note: remainder of annotations omitted.

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Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 MNSFSTSAFGPVAFSLGILLVLPAPFAPVPPGDSKDVAAPHROPPLTSSERIDKQIRYI 60
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 LDGISALRKETCNKSNMCESSKEALAEANLNLPKMAEKDGCFCQSGFNEETCLVKIITGLL 120
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Qy 61 LDGISALRKETCNKSNMCESSPEALAEANLNLPKMAEKDGCFCQSGFNEETCLVKIITGLL 120
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Db 121 EFVYLEYLNQRFESSEQARAVQSTKVLIOFLQKAKNLDATITPDPPTNASLLTKLQ 180
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Db 181 AQONWLEDMPTHLILRSKEFLQSLRALRQM 212
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
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RESULT      2      146621      #type complete
ENTRY       prointerleukin 6 - pig
TITLE       #formal_name Sus scrofa domestica #common_name domestic pig
ORGANISM    21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
DATE        16-Jul-1999

ACCESSIONS  146621
REFERENCE    Richards, C.; Saklatva, J.
#authors     Cytokine (1991) 3:269-276
#journal     Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA
#title       and Expression of mRNA in Synovial Fibroblasts In Vitro.
#cross-references MUID:91338547
#accession   146621
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#residues    1-212 ##label RIC
#cross-references GB:M86722; NID:g164624; PIDN:AAC37333.1; PID:g164625

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#superfamily interleukin-6
CLASSIFICATION #length 212 #molecular-weight 23880 #checksum 819
SUMMARY

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Db 61 LKISAMRKEMCEKEKENSKEVLAENLNLPKMAEKDGCFCQSGFNEETCLMRITGLV 120
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Qy 61 LDGISALRKETCNKSNMCESSPEALAEANLNLPKMAEKDGCFCQSGFNEETCLVKIITGLL 120
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Db 121 EFQIYLDYLOKYESKNGNVEAVQISTKALIQTLQKGNPKDATTNPPTNAGLLDKLQ 180
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Qy 121 EFVYLEYLNQRFESSEQARAVQSTKVLIOFLQKAKNLDATITPDPPTNASLLTKLQ 180
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Db 181 SQENWMKNTKIILRSLEDFLQSLRAIRIM 212
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Qy 181 AQONWLEDMPTHLILRSKEFLQSLRALRQM 212
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT      4
ENTRY       T09216      #type complete
TITLE       Interleukin-6 precursor - horse
ORGANISM    #formal_name Equus caballus #common_name domestic horse
DATE        11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change
ACCESSIONS  T09216
REFERENCE    Z16613
#authors     Swiderski, C.E.; Horohov, D.W.
#submission submitted to the EMBL Data Library, July 1996
#accession   T09216
#status      preliminary; translated from GB/EMBL/DDBJ
#molecule_type mRNA
#residues    1-208 ##label SWI
#cross-references EMBL:U64794; NID:g2654387; PID:g2654388

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#superfamily interleukin-6
KEYWORDS     cytokine; growth factor
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Best Local Similarity 60.4%; Pred. No. 3.60e-158;
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61 LDGISALRKETCNKSNMCESSPEALAEENNLNPKMAEKDGCFOGFGNQCETCLVKIITGLL 120
118 EFQIYLEYLQNEFKGEKNITKMTQISKVLQVILQMKMKNPE-VTTDPDTAKSKILLAKLH 176
121 EFQIYLEYLQNEFKGEKNITKMTQISKVLQVILQMKMKNPE-VTTDPDTAKSKILLAKLH 176
177 SONWLKNTTHLILRSLEDFLQSLRAVRIM 208
181 AQOWLEDMPTHLILRSLEDFLQSLRALRQM 212

RESULT 5
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TITLE Interleukin-6 precursor - bovine
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
ACCESSIONS A56610; S22162
REFERENCE A56610
#authors Droogmans, L.; Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.
#journal DNA Seq. (1992) 2:411-413
#title Nucleotide sequence of bovine interleukin-6 cDNA.
#cross-references MUID:93076003
#accession A56610
#status preliminary
#molecule_type mRNA
#residues 1-208 #label DRO
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#note sequence extracted from NCBI backbone (NCBIP:118917)
CLASSIFICATION #superfamily interleukin-6
KEYWORDS cytokine
SUMMARY #length 208 #molecular-weight 23758 #checksum 8010

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Matches 112; Conservative 48; Mismatches 46; Indels 4; Gaps 2;

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61 VDKISARKEICEKNDCESSKETLAENLNPKMAEKDGCFOGFGNQCETCLIRITAGLL 120
QY 61 LDGISALRKETCNKSNMCESSPEALAEENNLNPKMAEKDGCFOGFGNQCETCLVKIITGLL 120
121 EYQIYLDYLNQYEGNVDLRKNTIQLIQLKQIADL--ITTP--ATNTDLEKMQ 176
QY 121 EFQIYLEYLQNEFKGEKNITKMTQISKVLQVILQMKMKNPE-VTTDPDTAKSKILLAKLH 180
177 SSNEWKNAKIIILRNLENFLQSLRAIR 206
QY 181 AQOWLEDMPTHLILRSLEDFLQSLRALR 210

RESULT 6
ENTRY I46084 #type complete
TITLE Interleukin 6 - cat
ORGANISM #formal_name Felis silvestris catus #common_name domestic cat
DATE 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change
ACCESSIONS I46084
REFERENCE I46084
#authors Bradley, W.G.; Gibbs, C.; Kraus, L.; Good, R.A.; Day, N.K.
#journal Proc. Soc. Exp. Biol. Med. (1993) 204:301-305
#title Molecular cloning and characterization of a cDNA encoding feline interleukin-6.

#cross-references MUID:94052249
#accession I46084
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-207 #label BRA
#cross-references GB:L16914; NID:g438519; PIDN:AAA16620.1; PID:g438520
CLASSIFICATION #superfamily interleukin-6
SUMMARY #length 207 #molecular-weight 23212 #checksum 9069

Query Match 53.9%; Score 801; DB 2; Length 207;
Best Local Similarity 54.0%; Pred. No. 5.54e-130;
Matches 115; Conservative 48; Mismatches 43; Indels 7; Gaps 5;

Db 1 MNFLSTSAFSLAFSLGILLVAVATAPTPGLG--G-D-ATSNRLPLTPADKMEELIKYI 56
QY 1 MNSFSTSAFGVAFSLGILLVLPAAFPAPVPGEDSKDVAAPHRQPLTSSERIDKQIRYI 60
57 LGKISALKNEMCDNKNKCEDSKALAEENNLNPKLAEKDGCFOGFGNQCETCLIRITITGLQ 116
QY 61 LDGISALRKETCNKSNMCESSPEALAEENNLNPKMAEKDGCFOGFGNQCETCLVKIITGLL 120
117 EFQIYLEYLQNEFKGEKNITKMTQISKVLQVILQMKMKNPE-VTTDPDTAKSKILLAKLH 174
QY 121 EFQIYLEYLQNEFKGEKNITKMTQISKVLQVILQMKMKNPE-VTTDPDTAKSKILLAKLH 180
175 CSRRVAEAAHNNHLLRLRLEDFLQSLRAVRIM 207
QY 181 AQOWLEDMPTHLILRSLEDFLQSLRALRQM 212

RESULT 7
ENTRY S29549 #type complete
TITLE Interleukin-6 - sheep
ORGANISM #formal_name Ovis orientalis aries, Ovis ammon aries
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
ACCESSIONS S29549
REFERENCE S29549
#authors Ebrahimi, B.
#submission submitted to the EMBL Data Library, October 1992
#accession S29549
#status preliminary
#molecule_type mRNA
#residues 1-208 #label EBR
#cross-references EMBL:X68723
CLASSIFICATION #superfamily interleukin-6
SUMMARY #length 208 #molecular-weight 23526 #checksum 7927

Query Match 53.6%; Score 796; DB 1; Length 208;
Best Local Similarity 52.9%; Pred. No. 5.57e-129;
Matches 111; Conservative 47; Mismatches 48; Indels 4; Gaps 2;

Db 1 MNSRFTSAFSLAVSLGILLVMTSAFTPGPLGDEKNDTTPSRLLTTPKEALIKHI 60
QY 1 MNSFSTSAFGVAFSLGILLVLPAAFPAPVPGEDSKDVAAPHRQPLTSSERIDKQIRYI 60
61 VDKISARKEICEKNDCESSKETLAENLNPKMAEKDGCFOGFGNQCETCLIRITAGLL 120
QY 61 LDGISALRKETCNKSNMCESSPEALAEENNLNPKMAEKDGCFOGFGNQCETCLVKIITGLL 120
121 EYQIYLDYLNQYEGNVDLRKNTIQLIQLKQIADL--ITTP--ATHTDLEKMQ 176
QY 121 EFQIYLEYLQNEFKGEKNITKMTQISKVLQVILQMKMKNPE-VTTDPDTAKSKILLAKLH 180
177 SSNEWKNAKIIILRNLENFLQSLRAIR 206
QY 181 AQOWLEDMPTHLILRSLEDFLQSLRALR 210

RESULT 8
ENTRY ICMS6 #type complete
TITLE Interleukin-6 precursor - mouse
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ALTERNATE_NAMES B-cell hybridoma growth factor; B-cell stimulating factor 2;
                  hepatocyte-stimulating factor; IL-6; interferon beta-II;
                  interleukin-HP1; myeloid differentiation inducer MGI-2A;
                  plasmacytoma growth factor
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change
ACCESSIONS A30531; A27610; A30571; S01323; S12103; E34047; A26662;
            A40486; A60799; S10241; S38254
REFERENCE A30531
#authors Tanabe, O.; Akira, S.; Kamiya, T.; Wong, G.G.; Hirano, T.;
          Kishimoto, T.
#journal J. Immunol. (1988) 141:3875-3881
#title Genomic structure of the murine IL-6 gene. High degree
        conservation of potential regulatory sequences between
        mouse and human.
#cross-references MUID:89035525
#accession A30531
##molecule_type DNA
##residues 1-211 #label TAN
##cross-references GB:M20572; NID:g198369; PIDN:AAA39302.1; PID:g387386
REFERENCE A27610
#authors Van Snick, J.; Cayphas, S.; Szikora, J.P.; Renauld, J.C.; Van
          Roost, E.; Boon, T.; Simpson, R.J.
#journal Eur. J. Immunol. (1988) 18:193-197
#title cDNA cloning of murine interleukin-HP1: homology with human
        interleukin 6.
#cross-references MUID:88166883
#accession A27610
##molecule_type mRNA
##residues 1-211 #label VAN
##cross-references GB:X06203; NID:g52701; PIDN:CAA29560.1; PID:g52702
REFERENCE A30571
#authors Mock, B.A.; Nordan, R.P.; Justice, M.J.; Kozak, C.; Jenkins,
          N.A.; Copeland, N.G.; Clark, S.C.; Wong, G.G.; Rudikoff, S.
#journal J. Immunol. (1989) 142:1372-1376
#title The murine il-6 gene maps to the proximal region of
        chromosome 5.
#cross-references MUID:89124383
#accession A30571
##molecule_type mRNA
##residues 5-211 #label MOC
##cross-references GB:M24221; NID:g341131; PIDN:AAA68814.1; PID:g870699
REFERENCE S01323
#authors Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.
#journal Eur. J. Biochem. (1988) 176:187-197
#title Murine hybridoma/plasmacytoma growth factor. Complete
        amino-acid sequence and relation to human interleukin-6.
#cross-references MUID:88329059
#accession S01323
##molecule_type protein
##residues 25-166, 'X', 168-211 #label SIM
##note the sequence from Fig. 11 is inconsistent with that from
        Fig. 10 in having 103-Asn
REFERENCE S12103
#authors Grenett, H.E.; Fuentes, N.L.; Fuller, G.M.
#journal Nucleic Acids Res. (1990) 18:6455
#title Cloning and sequence analysis of the cDNA for murine
        interleukin-6.
#cross-references MUID:91057159
#accession S12103
##molecule_type mRNA
##residues 1-211 #label GRE
##cross-references EMBL:X54542; NID:g52727; PIDN:CAA38411.1; PID:g52728
REFERENCE A90157
#authors Jahnke, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson,
          R.J.
#journal Biochem. Biophys. Res. Commun. (1990) 166:139-145
#title Internal amino acid sequencing of proteins by in situ
        cyanogen bromide cleavage in polyacrylamide gels.
#cross-references MUID:90147691
#accession E34047
##molecule_type protein

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##residues 66-69, 'X', 71-75; 78-94; 128-148 #label JA5
REFERENCE A26662
#authors Van Snick, J.; Cayphas, S.; Vink, A.; Uyttenhove, C.; Coulie,
          P.G.; Rubira, M.R.; Simpson, R.J.
#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:9679-9683
#title Purification and NH2-terminal amino acid sequence of a
        T-cell-derived lymphokine with growth factor activity for
        B-cell hybridomas.
#cross-references MUID:87092311
#accession A26662
##molecule_type protein
##residues 25-39, 'X', 41-42, 'X', 44-45 #label VSN
REFERENCE A40486
#authors Chiu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.
#journal Proc. Natl. Acad. Sci. U.S.A. (1988) 85:7099-7103
#title Multiple biological activities are expressed by a mouse
        interleukin 6 cDNA clone isolated from bone marrow stromal
        cells.
#cross-references MUID:89017145
#accession A40486
##molecule_type mRNA
##residues 1-211 #label CHI
##cross-references GB:J03783; NID:g198367; PIDN:AAA39301.1; PID:g309410
REFERENCE A60799
#authors Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.;
          Wolf, S.F.; Kamen, R.; Sachs, L.
#journal Blood (1988) 72:2070-2073
#title The myeloid blood cell differentiation-inducing protein
        MGI-2A is interleukin-6.
#cross-references MUID:89062753
#accession A60799
##molecule_type protein
##residues 77-98 #label SHA
REFERENCE S10241
#authors Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
#journal J. Exp. Med. (1990) 171:965-970
#title DNA rearrangement and constitutive expression of the
        interleukin 6 gene in a mouse plasmacytoma.
#cross-references MUID:90171860
#accession S10241
##status preliminary
##molecule_type DNA
##residues 1-6 #label BLA
##cross-references EMBL:X51457; NID:g49738; PIDN:CAA35824.1; PID:g581860
REFERENCE S38254
#authors Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson,
          R.J.
#journal Eur. J. Biochem. (1993) 217:53-59
#title Specific covalent modification of the tryptophan residues in
        murine interleukin-6. Effect on biological activity and
        conformational stability.
#cross-references MUID:94039075
#accession S38254
##status preliminary
##molecule_type protein
##residues 38-60; 75, 'X', 77-79; 176-203 #label ZHA
GENETICS
#gene il-6
#map_position 5
#introns 7/1; 68/3; 106/3; 156/3
CLASSIFICATION #superfamily interleukin-6
KEYWORDS Castleman's disease; cytokine; growth factor;
          immunoregulation; lymphokine; macrophage; rheumatoid
          arthritis
FEATURE
1-24 #domain signal sequence #status predicted #label SIG\
25-211 #product interleukin-6 #status experimental #label MAT
SUMMARY
#length 211 #molecular-weight 24384 #checksum 5652
Query Match 43.8%; Score 650; DB 1; Length 211;
Best Local Similarity 41.8%; Pred. No. 6.59e-100;
Matches 89; Conservative 55; Mismatches 64; Indels 5; Gaps 5;

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Db 1 MKFLSARDHPVAF-LGLMLVTATAPPTSOVRGDFTE-TTPNR-PVYTTSOVGLITH 57
QY 1 MNSFSTSAFGPVAFSLGULLVLPAFPAP-VPPGEDSKDVAAPHRQPLTSSERIDKQIRY 59

Db 58 VLWEIVEMRKELCNGNSDCMNDALAEENNLKLPFIQRNDGICYGYNQIECLLKISGL 117
QY 60 ILDGISALRKETCNKSNMCESSPEALAEENNLKPKMAEKDGCFOGFEETCLVKIITGL 119

Db 118 LEVHSYLEYKMNKDKKARVLDQRTETLIHFQNVQKDLHKIVLPTPTSNALLTDK 177
QY 120 LEFEVYLEYLNRF-ESSEQARAVQMSTKVLIQLOKAKNLDALTTPDPTTNASLLTK 178

Db 178 LESQEWLTKTIQIFILKSLEELFKVTLRSTRQ 210
QY 179 LQAQNWLEDMPHTLIILRSKLEFLQSLRALRQ 211

RESULT 9
ENTRY #34247 #type complete
TITLE interleukin-6 precursor - rat
ALTERNATE_NAMES IL-6
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 16-Jul-1999
ACCESSIONS A34247
REFERENCE Northemann, W.; Braciak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
#journal J. Biol. Chem. (1989) 264:16072-16082
#title Structure of the rat interleukin 6 gene and its expression in macrophage-derived cells.
#cross-references MUID:89380206
#accession A34247
#status preliminary
#molecule_type mRNA
#residues 1-211 ##label NOR
#cross-references GB:M26744; NID:g204915; PIDN:AAA7659.1; PID:g204916
CLASSIFICATION #superfamily interleukin-6
KEYWORDS cytokine; growth factor; immunoregulation; lymphokine; macrophage
SUMMARY #length 211 #molecular-weight 24357 #checksum 5864

Query Match 43.2%; Score 642; DB 2; Length 211;
Best Local Similarity 40.8%; Pred. No. 2.51e-98;
Matches 87; Conservative 60; Mismatches 61; Indels 5; Gaps 5;

Db 1 MKFLSARDHPVAF-LGLMLVTATAPPTSOVRGDFTE-TTPNR-PVYTTSOVGLITH 57
QY 1 MNSFSTSAFGPVAFSLGULLVLPAFPAP-VPPGEDSKDVAAPHRQPLTSSERIDKQIRY 59

Db 58 VLWEIVEMRKELCNGNSDCMNDALAEENNLKLPFIQRNDGICYGYNQIECLLKISGL 117
QY 60 ILDGISALRKETCNKSNMCESSPEALAEENNLKPKMAEKDGCFOGFEETCLVKIITGL 119

Db 118 LEFEVYLEYLNRF-ESSEQARAVQMSTKVLIQLOKAKNLDALTTPDPTTNASLLTK 177
QY 120 LEFEVYLEYLNRF-ESSEQARAVQMSTKVLIQLOKAKNLDALTTPDPTTNASLLTK 178

Db 178 LESQEWLTKTIQIFILKSLEELFKVTLRSTRQ 210
QY 179 LQAQNWLEDMPHTLIILRSKLEFLQSLRALRQ 211

RESULT 10
ENTRY #A42247 #type complete
TITLE myelomonocytic growth factor precursor - chicken
ALTERNATE_NAMES colony-stimulating factor cmf
ORGANISM #formal_name Gallus gallus #common_name chicken
DATE 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
ACCESSIONS A42247; S03633
REFERENCE Sterneck, E.; Blattner, C.; Graf, T.; Leutz, A.

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#journal Mol. Cell. Biol. (1992) 12:1728-1735
#title Structure of the chicken myelomonocytic growth factor gene and specific activation of its promoter in avian myelomonocytic cells by protein kinases.
#cross-references MUID:92195319
#accession A42247
#status preliminary
#molecule_type DNA
#residues 1-201 ##label STE
#note sequence extracted from NCBI backbone (NCBIN:89832, NCBIP:89836)

REFERENCE S03633
#authors Leutz, A.; Damm, K.; Sterneck, E.; Kowenz, E.; Ness, S.; Frank, R.; Gausepohl, H.; Pan, Y.C.E.; Smart, J.; Hayman, M.; Graf, T.
#journal EMBO J. (1989) 8:175-181
#title Molecular cloning of the chicken myelomonocytic growth factor (CMGF) reveals relationship to interleukin 6 and granulocyte colony stimulating factor.
#cross-references MUID:89231616
#accession S03633
#molecule_type mRNA
#residues 1-201 ##label LEU
#cross-references EMBL:X14477; NID:g63596; PIDN:CAA32639.1; PID:g63597
CLASSIFICATION #superfamily interleukin-6
KEYWORDS glycoprotein
FEATURE #domain signal sequence #status predicted #label SIG\
1-23 #product myelomonocytic growth factor #status predicted
24-201 #label MAT\
123,137 #binding site carbohydrate (Asn) (covalent) #status predicted

SUMMARY #length 201 #molecular-weight 22373 #checksum 9000

Query Match 11.2%; Score 166; DB 2; Length 201;
Best Local Similarity 22.8%; Pred. No. 6.08e-10;
Matches 45; Conservative 43; Mismatches 103; Indels 6; Gaps 5;

Db 8 LALALVLGAPQQA-LH-CAPLAELSGDHFOLFHLKNE-LFTRKIRGDVAALQAVCDTF 64
QY 16 LGLLLVLPAAAPPAPPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKS 75

Db 65 QLCETEELQLVQDPDHLVQ-APLDQCHKRGFQAEVCTQIRAGLHAYHDSIGAVLRLLPN 123
QY 76 NMCESSPEALAEENNLKPKMAEKDGCFOGFEETCLVKIITGLLEFEVYLEYLNRFES 135

Db 124 HTTIVETLQDAANLSSNIQQOMEDLGLDVTLPAPORSPPPTSGFPQ--QQVGGFPIL 181
QY 136 SEQARAVQMSTKVLIQLOKAKNLDALTTPDPTTNASLLTKLQAOQNQWLEDMPTHLIL 195

Db 182 ANFORFLETAVRALRHL 198
QY 196 RSLKEFLQSLRALRQM 212

RESULT 11
ENTRY #T09255 #type fragment
TITLE granulocyte colony-stimulating factor precursor - cat
ORGANISM #formal_name Felis silvestris catus #common_name domestic cat
DATE 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
ACCESSIONS T09255
REFERENCE Z16630
#authors Dunham, S.P.; Onions, D.E.
#submission submitted to the EMBL Data Library, September 1996
#description Cloning, sequence and expression of feline granulocyte colony stimulating factor.
#accession T09255
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-194 ##label DUN
#cross-references EMBL:Y08558; NID:e1006755; PID:e270012

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[illegible]

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#title      Structural studies on the murine granulocyte
             colony-stimulating factor.
#cross-references MUID:88106998
#accession   S02493
#status      preliminary
#molecule_type protein
#residues    31-34,'X',36-43;48-51,'X',53-57,'X',60-71;159-164,'X',
             166-176;183-198,'X',200 #label SIM

GENETICS
#introns     14/1: 71/3; 107/3; 156/3
CLASSIFICATION #superfamily interleukin-6
KEYWORDS       cytokine; growth factor; macrophage; monomer
SUMMARY        #length 208 #molecular-weight 22421 #checksum 6232

Query Match      7.3%; Score 108; DB 2; Length 208;
Best Local Similarity 27.0%; Pred. No. 1.40e-01;
Matches 20; Conservative 17; Mismatches 36; Indels 1; Gaps 1;

Db 56 QVRKIQAGSVLLEQLCATYKLCHPPELVLLGHSIGIPK-ASLSGCSQALQOQCISQL 114
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Qy 56 QIRYILDGISALRKETCNKSNMCESSPEALAEENLNLPKMAEKDGCFCQSGFNEETCLVKI 115
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db 115 HSGLCYQGLLQAL 128
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Qy 116 ITGLEFEVYLEYL 129

RESULT 15
ENTRY   T01430      #type complete
TITLE   syntaxin homolog T2H3.1 - Arabidopsis thaliana
ORGANISM #formal_name Arabidopsis thaliana #common_name mouse-ear
          cress
DATE     12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change
          24-Mar-1999
ACCESSIONS T01430
REFERENCE   Z14324
          #authors   Kalicki, J.; Gibson, A.
          #submission submitted to the EMBL Data Library, August 1998
          #description The sequence of A. thaliana T2H3.
          #accession  T01430
          #status     translated from GB/EMBL/DBJ
          #molecule_type DNA
          #residues    1-287 #label KAL
          #cross-references EMBL:AF075597; NID:g3298610; PID:g3377798
          #experimental_source cultivar Columbia

GENETICS
#map_position 4
#introns       64/2; 156/3; 186/3; 211/3; 237/3; 259/3
#note          T2H3.1
SUMMARY        #length 287 #molecular-weight 32420 #checksum 2900

Query Match      7.3%; Score 109; DB 2; Length 287;
Best Local Similarity 23.8%; Pred. No. 1.04e-01;
Matches 20; Conservative 24; Mismatches 37; Indels 3; Gaps 3;

Db 105 LMPFTGDNKGIRHEVEMLTHTITLLRKSEKRLQMLTRGPFSESNLRKNVQSRSLATDLQ 164
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 129 LQNRFESEEQARAVQSTKVLIQFLQKAKNLDAITTPDTTNASLLTLKIQ-AQNQWLE 187
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db 165 NLSMELR-RKOSTYIKR-LQOQKE 186
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Qy 188 DMPHTLILRLSLEFLQSLRALRQ 211
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CC ZIP: 10014
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC Compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/231,575
CC FILING DATE: 22-APR-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/918,181
CC FILING DATE: 23-JUL-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Sheets, Eric J.
CC REGISTRATION NUMBER: 30,326
CC REFERENCE/DOCKET NUMBER: FOW-2
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 212-645-1405
CC TELEFAX: 212-645-2054
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 185 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 185 AA; 20965 MW; 169089 CN;

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Best Local Similarity 97.3%; Pred. No. 4,91e-91;
Matches 180; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 APVPPGDSKDVAAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKNMCESSKEALAE 60
QY 28 APVPPGDSKDVAAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKNMCESSPEALAE 87

Db 61 NNILNPKMAEKDCGFSQSGNEETCLVKIITGLLEFEVYLEYLQNRFPESSEQARAVOMST 120
QY 88 NNILNPKMAEKDCGFSQSGNEETCLVKIITGLLEFEVYLEYLQNRFPESSEQARAVOMST 147

Db 121 KVLQFLQKAKNLDATTPDPTTNASLLTKLQAQNWLEDMPTHLILRSKFEFLQSLR 180
QY 148 KVLQFLQKAKNLDATTPDPTTNASLLTKLQAQNWLEDMPTHLILRSKFEFLQSLR 207

Db 181 ALRQM 185
QY 208 ALRQM 212

RESULT 9
ID US-07-632-070B-1 STANDARD; PRT; 185 AA.
XX
AC xxxxxx
XX
DT
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DE
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Sequence 1, Application US/07632070B
XX
Sequence 1, Application US/07632070B
CC Patent No. 5264209
CC GENERAL INFORMATION:
CC APPLICANT: Mikayama, Toshihumi
CC APPLICANT: APPLICANT: Kadoya, Toshihiko
CC APPLICANT: APPLICANT: Kakitani, Makoto
CC APPLICANT: APPLICANT: Inoue, Hideo
CC TITLE OF INVENTION: Modified hil-6
CC NUMBER OF SEQUENCES: 3
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein,
CC ADDRESSEE: Murray & Bicknell
CC STREET: 20 South Clark Street, Suite 2100
CC CITY: Chicago
CC STATE: Illinois

CC COUNTRY: United States of America
CC ZIP: 60603
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
CC COMPUTER: IBM COMPATIBLE
CC OPERATING SYSTEM: MS-DOS
CC SOFTWARE: NBI
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/632,070B
CC FILING DATE: 19901221
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 2-32273
CC FILING DATE: 13 FEB 1990
CC APPLICATION NUMBER: JP 2-222353
CC FILING DATE: 22 AUG 90
CC APPLICATION NUMBER: JP 2-250460
CC FILING DATE: 21 SEPT 1990
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 185
CC TYPE: AMINO ACID
CC STRANDEDNESS:
CC TOPOLOGY: Linear
CC SEQUENCE 185 AA; 20981 MW; 169252 CN;

Query Match 84.6%; Score 1257; DB 1; Length 185;
Best Local Similarity 97.3%; Pred. No. 8,64e-91;
Matches 180; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 APVPPGDSKDVAAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKNMCESSKEALAE 60
QY 28 APVPPGDSKDVAAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKNMCESSPEALAE 87

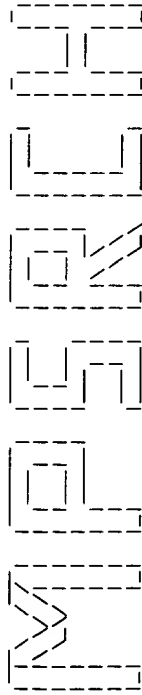
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QY 88 NNILNPKMAEKDCGFSQSGNEETCLVKIITGLLEFEVYLEYLQNRFPESSEQARAVOMST 147

Db 121 KVLQFLQKAKNLDATTPDPTTNASLLTKLQAQNWLEDMPTHLILRSKFEFLQSLR 180
QY 148 KVLQFLQKAKNLDATTPDPTTNASLLTKLQAQNWLEDMPTHLILRSKFEFLQSLR 207

Db 181 ALRQM 185
QY 208 ALRQM 212

RESULT 10
ID 5186931-2 STANDARD; PRT; 185 AA.
XX
AC xxxxxx
XX
DT
XX
DE Patent No. 5186931
XX
Patent No. 5186931
CC APPLICANT: Kishimoto, Tadamitsu; Hirano, Toshio; Akiyama, Yukio;
CC Okano, Akira; Matsui, Hiroshi; Takahara, Yoshiyuki
CC TITLE OF INVENTION: COMPOSITION AND METHOD FOR SUPPORTING BONE
CC MARROW TRANSPLANTATION
CC NUMBER OF SEQUENCES: 2
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/366,866
CC FILING DATE: 15-JUN-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 81,746
CC FILING DATE: 05-AUG-1987
CC SEQ ID NO: 2:
CC LENGTH: 185
CC SEQUENCE 185 AA; 20981 MW; 169252 CN;

Query Match 84.6%; Score 1257; DB 5; Length 185;



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Aug 10 16:25:48 2000; MasPar time 8.44 Seconds
Tabular output not generated. 594.691 Million cell updates/sec

Title: >US-09-142-471-5
Description: (1-212) from US09142471.pap
Perfect Score: 1485
Sequence: 1 MNSFSTAFGVPVAFSLGILL.....LILRSKLEFLQRSRLALRQ M 212

Scoring table: PAM 150
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq36
1:geneseq

Statistics: Mean 32.908; Variance 163.071; scale 0.202

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description	Pred. No.
1	1485	100.0	212	1	W35878 Human interleukin-6 (I	3.46e-114
2	1485	100.0	212	1	W33843 Human interleukin-6 (I	3.46e-114
3	1446	97.4	212	1	R49249 Sequence of human B-ce	7.79e-111
4	1446	97.4	212	1	P80269 Recombinant interleuki	7.79e-111
5	1446	97.4	212	1	P90047 pBSF2-L8 sequence	7.79e-111
6	1446	97.4	212	1	P70238 Interferon-beta 2a.	7.79e-111
7	1446	97.4	212	1	P90436 Interferon-beta-2.	7.79e-111
8	1446	97.4	212	1	P90469 Interleukin-6	7.79e-111
9	1446	97.4	212	1	R72317 Interferon-beta2A.	7.79e-111
10	1446	97.4	212	1	R33430 IFN-beta-2a.	7.79e-111
11	1446	97.4	212	1	R05415 Human B-cell different	7.79e-111
12	1446	97.4	212	1	R49041 Human interleukin-6.	7.79e-111
13	1446	97.4	212	1	R34726 Human IL-6 (for modifi	7.79e-111
14	1446	97.4	212	1	P90371 pBSF2-L8	7.79e-111
15	1443	97.2	212	1	P81156 Human B-cell different	1.41e-110
16	1441	97.0	212	1	P82577 Leader sequence of	2.10e-110
17	1441	97.0	212	1	P81176 Sequence of the BSF-2	2.10e-110
18	1441	97.0	212	1	P90121 Human lymphocyte recep	2.10e-110
19	1437	96.8	212	1	R33384 Cytokine hIL-6.	4.62e-110
20	1421	95.7	212	1	R12521 B cell differentiation	1.10e-108
21	1410	94.9	211	1	R25279 Mutant human Bcdf.	9.66e-108
22	1280	86.2	188	1	W95011 Human interleukin-6 (I	1.39e-96
23	1273	85.7	208	1	P81160 Polypeptide with B-cell	5.53e-96

ALIGNMENTS

RESULT 1

ID	W35878	standard; protein; 212 AA.	208	1	P94755	Sequence of variant of	1.81e-95
AC	W35878		543	1	R03164	Chimeric sIL-6R/IL-6 p	1.81e-95
DT	27-APR-1998	(first entry)	185	1	R45718	Full length interleuki	3.26e-95
DE	Human interleukin-6 (IL-6)	mutein polypeptide.	185	1	W13999	Interleukin-6 receptor	3.98e-95
KW	Interleukin-6; IL-6;	mutein; antagonist; human; mutation; treatment;	185	1	R45720	Full length interleuki	7.19e-95
KW	plasmocytoma; myeloma; osteoporosis; autoimmune disease.		185	1	P81159	Polypeptide with B-cel	1.30e-94
OS	Synthetic.		185	1	R05275	Segment of human B cel	1.30e-94
OS	Homo sapiens.		185	1	R68624	Ala-Bcdf.	1.30e-94
FH	Key	Location/Qualifiers	185	1	R45717	Full length interleuki	1.30e-94
FT	Peptide	1..28	185	1	R75765	Human interleukin-6.	1.30e-94
FT	Protein	/note= "signal peptide"	187	1	P80270	Recombinant interleuki	1.30e-94
FT	Misc_difference 82	/note= "mature protein"	184	1	W02609	hIL-6 protein.	1.30e-94
FT	Misc_difference 187	/label= K82P	184	1	R20783	Interleukin-6.	2.86e-94
FT	Misc_difference 190	/note= "wild type Lys is replaced by Pro"	185	1	R03914	Polypeptide with human	2.86e-94
FT	Misc_difference 198	/label= Q187E	184	1	R55256	Interleukin 6.	2.86e-94
FT	Misc_difference 198	/note= "wild type Gln is replaced by Glu"	185	1	R06532	Human B-cell stimulator	2.86e-94
FT	Misc_difference 198	/label= T190P	185	1	P91015	Synthetic interleukin-	2.86e-94
FT	Misc_difference 204	/note= "wild type Thr is replaced by Pro"	185	1	W00130	Human interleukin-6 fr	2.86e-94
FT	Misc_difference 204	/label= S204R	185	1	R45719	Full length interleuki	2.86e-94
FT	Misc_difference 204	/note= "wild type Ser is replaced by Arg"	500	1	W36847	Human fusion polypepti	2.86e-94
FT	Misc_difference 204	/label= S204R	525	1	W36846	Human fusion polypepti	2.86e-94

WO9738103-Al.
16-OCT-1997.
09-APR-1996; E01506.
09-APR-1996; WO-E01506.
(ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Ehlers M, Grotzinger J, Rose-John S;
WPI: 97-512720/47.
New interleukin-6 mutein polypeptides - useful as IL-6 antagonists
for treating e.g. plasmocytoma/myeloma, osteoporosis and neoplastic
and autoimmune diseases.
Claim 1; Pages 15-16; 38pp; English.
This is a interleukin-6 (IL-6) mutein polypeptide. This IL-6 mutein
comprises a mature protein of 184 amino acids. This polypeptide is
created by point mutations on the wild-type human IL-6, at positions
54, 159, 162, 170,176 of the mature human IL-6. The DNA sequence encoding
this IL-6 mutein and the sequences encoding variants having the same
activity resulting from the degeneracy of the genetic code or point
mutations can be used to transform a host cell. The IL-6 mutein can act

as IL-6 antagonist. This polypeptide and its fragments can be used for treating diseases in which IL-6 has a pathogenic action such as plasmacytoma myeloma, osteoporosis and neoplastic and autoimmune diseases. 212 AA;

Query Match 100.0%; Score 1485; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.46e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
QY 1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
Db 61 LDGTSALKETCNKSNMCESSPEALAEENNLPMKAEKDCGFCQGFNEETCLVKIITGLL 120
QY 61 LDGTSALKETCNKSNMCESSPEALAEENNLPMKAEKDCGFCQGFNEETCLVKIITGLL 120
Db 121 EFVYLYLQNRFFESSEQARAVQSTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQ 180
QY 121 EFVYLYLQNRFFESSEQARAVQSTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQ 180
Db 181 AQNWLEDMPTHLILRSKEFLQSLRALROM 212
QY 181 AQNWLEDMPTHLILRSKEFLQSLRALROM 212

RESULT 2
ID W33643 standard; protein; 212 AA.
AC W33643;
DT 27-APR-1998 (first entry)
DE Human interleukin-6 (IL-6) mutein polypeptide.
KW Interleukin-6; IL-6; mutein; antagonist; human; mutation; treatment;
KW plasmacytoma; myeloma; osteoporosis; autoimmune disease.
OS Synthetic.
FS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..28
FT /note= "signal peptide"
FT Protein 29..212
FT /note= "mature protein"
FT Misc_difference 82
FT /label= K82P
FT /note= "wild type Lys is replaced by Pro"
FT Misc_difference 187
FT /label= Q187E
FT /note= "wild type Gln is replaced by Glu"
FT Misc_difference 190
FT /label= T190P
FT /note= "wild type Thr is replaced by Pro"
FT Misc_difference 198
FT /label= F198L
FT /note= "wild type Phe is replaced by Leu"
FT Misc_difference 204
FT /label= S204R
FT /note= "wild type Ser is replaced by Arg"
W09738104-A1.
16-OCT-1997.
PD 08-APR-1997; E01736
PF 09-APR-1996; W0-E01506.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
PI Ehlers M, Grotzinger J, Rose-John S;
DR WPI; 97-512721/47.
PT New interleukin-6 mutein polypeptide - useful as IL-6 antagonist for
PT treating e.g. plasmacytoma/myeloma, osteoporosis and neoplastic and
PT autoimmune diseases
PS Claim 1; Pages 15-16; 37pp; English.
CC This is a interleukin-6 (IL-6) mutein polypeptide. This IL-6 mutein
CC comprises a mature protein of 184 amino acids. This polypeptide is
CC created by point mutations on the wild-type human IL-6 at positions
CC 54, 159, 162, 170, 176 of the mature human IL-6. The DNA sequence encoding
CC this IL-6 mutein and the sequences encoding variants having the same
CC activity resulting from the degeneracy of the genetic code or point

mutations can be used to transform a host cell. The IL-6 mutein can act as IL-6 antagonist. This polypeptide and its fragments can be used for treating diseases in which IL-6 has a pathogenic action such as plasmacytoma myeloma, osteoporosis and neoplastic and autoimmune diseases. 212 AA;

Query Match 100.0%; Score 1485; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.46e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
QY 1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
Db 61 LDGTSALKETCNKSNMCESSPEALAEENNLPMKAEKDCGFCQGFNEETCLVKIITGLL 120
QY 61 LDGTSALKETCNKSNMCESSPEALAEENNLPMKAEKDCGFCQGFNEETCLVKIITGLL 120
Db 121 EFVYLYLQNRFFESSEQARAVQSTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQ 180
QY 121 EFVYLYLQNRFFESSEQARAVQSTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQ 180
Db 181 AQNWLEDMPTHLILRSKEFLQSLRALROM 212
QY 181 AQNWLEDMPTHLILRSKEFLQSLRALROM 212

RESULT 3
ID R49249 standard; Protein; 212 AA.
AC R49249;
DT 15-SEP-1994 (first entry)
DE Sequence of human B-cell differentiation factor (BCDF) encoded by
DE cDNA.
KW B-cell differentiation factor; BCDF; antitumour; antiviral;
KW lymphokine.
OS Homo sapiens.
PN EP-585957-A-
PD 09-MAR-1994.
PF 06-AUG-1987; 111409.
PR 06-AUG-1986; JP-184858.
PR 27-AUG-1986; JP-200433.
PR 18-DEC-1986; JP-302699.
PR 13-MAY-1987; JP-116332.
PA (AJIN) AJINOMOTO KK.
PA (KISH) KISHIMOTO T.
PI Akiyama Y, Hirano T, Kishimoto T, Matsui H, Okano A;
PI Takahara Y;
DR WPI; 94-076278/10.
DR N-PSDB; Q56265.
PT New non-glycosylated human B-cell differentiation factor -
PT lacking signal sequence and produced in bacteria, useful as
PT immuno therapeutic for stimulating antibody prodn, treating
PT cancer etc, also DNA encoding it
PS Claim 2; Fig 5; 63pp; English.
CC Human T cells transformed by human T cell leukaemia virus (HTLV)
CC produce BCDF which has an activity of 5x10(6) units/ml or more. For
CC its prep., RNA is extracted from human T cell line VT-1 (IFO 50096)
CC and used to construct a cDNA library. Oligos are constructed from
CC known N-terminal sequence of BCDF and used to screen the library.
CC One positive clone, contg. plasmid bpsr2-38, was selected and
CC sequenced; it includes the codons for an additional 28 AA N-terminal
CC region. A polypeptide corresp. to AAs 28-212 of R49249, and a
CC recombinant DNA comprising a gene encoding it are claimed.
SQ Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;
Best Local Similarity 97.6%; Pred. No. 7.79e-111;
Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
QY 1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60

RESULT 5
ID - p90047 standard; protein; 212 AA.

disclosure; Fig. 1A-B; English.
The protein has interferon activity. It inhibits viral replication and cytopathic effect and induces the proteins typical of the biological response of human cells to interferon. It is useful for influencing cell growth and differentiation, esp. during terminal differentiation of tumour cells and for inhibiting fibroblast proliferation and to prevent sclerosis after infection. The protein is also useful in the fields of inflammation acute-phase response or regulation of cell proliferation.
Sequence 212 AA:

Query Match 97.4%; Score 1446; DB 1; Length 212;
Best Local Similarity 97.6%; Pred. No. 7.79e-111;
Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYI 60
 QY 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYI 60
 Db 61 LDGIALRKETCNKSNMCESSKEALAEANNLPLKMAEKDGCFCQSGFNEETCLVKIITGLL 120
 QY 61 LDGIALRKETCNKSNMCESSPEALAEANNLPLKMAEKDGCFCQSGFNEETCLVKIITGLL 120
 Db 121 EFVYLEYLQNRFESEEQARAVQSTKVLQFLOKAKNLDATTPDPTTNASLLTKLQ 180
 QY 121 EFVYLEYLQNRFESEEQARAVQSTKVLQFLOKAKNLDATTPDPTTNASLLTKLQ 180
 Db 181 AQONQLDMPTHLILRSKFQSSLRALQRM 212
 QY 181 AQONQLDMPTHLILRSKFQSSLRALQRM 212

RESULT 7
 ID P90436 standard; peptide; 212 AA.
 AC P90436;
 DT 20-OCT-1989 (first entry)
 DE Interferon-beta-2.
 KW Interferon-beta 2; monoclonal antibodies; human;
 KW acute myelogenous leukaemia; breast cancer; bacterial and
 KW parasitic diseases; bone marrow transplants.
 OS Homo sapiens (human)
 FH EP-326120-A.
 PN 02-AUG-1989.
 PF 25-JAN-1989; 101295.
 PR 26-JAN-1988; IL-088376.
 PA (YEDA) Yeda Research and Dev Co Ltd.
 PI Revel M; Rubinstein M; Moriy Y; Chen L; Novick D; Michalewicz R.
 DR WPI: 89-222084/31.
 DR N-PSDB; N90377.
 PT Monoclonal antibody to human interferon-beta-2
 PT - produced by hybridoma cell line and useful for leukaemia
 PT treatment etc.
 PS Disclosure; fig 1; 26 pp; English.
 SC Interferon-beta-2 (see N90377). Used to make
 CC monoclonal antibodies, and in the treatment of the diseases
 CC in KW above.
 SQ Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;
 Best Local Similarity 97.6%; Pred. No. 7.79e-111;
 Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Db 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYI 60
 QY 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYI 60
 Db 61 LDGIALRKETCNKSNMCESSKEALAEANNLPLKMAEKDGCFCQSGFNEETCLVKIITGLL 120
 QY 61 LDGIALRKETCNKSNMCESSPEALAEANNLPLKMAEKDGCFCQSGFNEETCLVKIITGLL 120
 Db 121 EFVYLEYLQNRFESEEQARAVQSTKVLQFLOKAKNLDATTPDPTTNASLLTKLQ 180
 QY 121 EFVYLEYLQNRFESEEQARAVQSTKVLQFLOKAKNLDATTPDPTTNASLLTKLQ 180
 Db 181 AQONQLDMPTHLILRSKFQSSLRALQRM 212
 QY 181 AQONQLDMPTHLILRSKFQSSLRALQRM 212

RESULT 8
 ID P90469 standard; protein; 212 AA.
 AC P90469;
 DT 1-NOV-1989 (first entry)
 DE Interleukin-6
 KW Interleukin-6; lysine-depleted variant;
 KW site-directed mutagenesis; human.

OS Homo sapiens
 PN W0905824-A.
 PD 29-JUN-1989.
 PF 22-DEC-1988; U04633.
 PR 23-DEC-1987; US-137043.
 PA (GENE) Genetics Inst Inc.
 PI Shaw G;
 DR WPI: 89-206594/28.
 DR N-PSDB; N90255.
 PT New lysine depleted variants of polypeptide
 PT - opt. modified with hydrophilic residues,
 PT biologically active but with altered solubility, stability etc.
 PS Disclosure; fig 3; 35pp; English.
 CC DNA of interleukin-6 (see corresp. N90255). Used in the patent
 CC to create lysine depleted variants by site-directed mutagenesis,
 CC or synthesis.
 SQ Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;
 Best Local Similarity 97.6%; Pred. No. 7.79e-111;
 Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Db 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYI 60
 QY 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYI 60
 Db 61 LDGIALRKETCNKSNMCESSKEALAEANNLPLKMAEKDGCFCQSGFNEETCLVKIITGLL 120
 QY 61 LDGIALRKETCNKSNMCESSPEALAEANNLPLKMAEKDGCFCQSGFNEETCLVKIITGLL 120
 Db 121 EFVYLEYLQNRFESEEQARAVQSTKVLQFLOKAKNLDATTPDPTTNASLLTKLQ 180
 QY 121 EFVYLEYLQNRFESEEQARAVQSTKVLQFLOKAKNLDATTPDPTTNASLLTKLQ 180
 Db 181 AQONQLDMPTHLILRSKFQSSLRALQRM 212
 QY 181 AQONQLDMPTHLILRSKFQSSLRALQRM 212

RESULT 9
 ID R72317 standard; Protein; 212 AA.
 AC R72317;
 DT 14-NOV-1995 (first entry)
 DE Interferon-beta2A.
 KW biologically active; interferon-beta2A; IFN-beta2A; cell growth;
 KW terminal differentiation; cancer; inhibit fibroblast proliferation.
 OS Homo sapiens.
 PN EP-645452-A.
 PD 29-MAR-1995.
 PF 10-OCT-1986; 114478.
 PR 14-OCT-1985; IL-076714.
 PR 08-MAY-1986; US-860883.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Revel M, Zilberstein A;
 DR WPI: 95-124593/17.
 DR N-PSDB; Q86523.
 PT A DNA sequence encoding active interferon beta2A - used in the
 PT prodn. of the protein for the treatment of cancer, by inhibition
 PT of fibroblast proliferation
 PS Claim 1; Fig 1; 17pp; English.
 CC Biologically active interferon-beta2A (IFN-beta2A), including the
 CC N-terminus of the mature protein, may be used to influence cell growth
 CC and differentiation esp. terminal differentiation of cancer cells and
 CC to inhibit fibroblast proliferation preventing sclerosis after
 CC infection.
 SQ Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;
 Best Local Similarity 97.6%; Pred. No. 7.79e-111;
 Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Db 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYI 60
 QY 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYI 60

QY 1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGDSKDVAAAPHRQPLTSERIDKQIRYI 60

Db 61 LDGISALRKETCNKSNMCSSKEALAEENLNLPKMAEKDGCFCFSGFNEETCLVKIITGLL 120

QY 61 LDGISALRKETCNKSNMCSSKEALAEENLNLPKMAEKDGCFCFSGFNEETCLVKIITGLL 120

Db 121 EFVYLEYLQNRFESEEQARAVOMSTKVLIQFLQKAKNLDATITPDPPTNASLTKLQ 180

QY 121 EFVYLEYLQNRFESEEQARAVOMSTKVLIQFLQKAKNLDATITPDPPTNASLTKLQ 180

Db 181 AQNWQDMTHLILRSFKFLOSLRALRQM 212

QY 181 AQNWQDMTHLILRSFKFLOSLRALRQM 212

RESULT 10

ID R33430 standard; Protein; 212 AA.

AC R33430;

DT 28-JUL-1993 (first entry)

DE IFN-beta-2a.

KW Interferon; IFN; pharmaceutical; inflammation; acute phase response; regulation; cell; proliferation; inhibition; fibroblast; sclerosis; infection; antiviral; antitumor; human; IFN-beta-1; IFN-beta-2; IFN-beta-2a; IFN-beta-2b.

KW IFN-beta-2a; IFN-beta-2b.

OS Homo sapiens.

PN EP-536520-A.

PD 14-APR-1993.

PF 10-OCT-1986; 114478.

PR 14-OCT-1985; IL-076714.

PR 08-MAY-1986; US-860883.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Revel M, Zilberstein A;

DR WPI: 93-118821/15.

DR N-PSDB: Q39582.

PT New compsn. contg. human interferon-beta 2A - for treating inflammation and acute phase response, regulating cell proliferation, etc.

PT proliferation, etc.

PS Disclosure; Fig 1; 16pp; English.

CC This sequence represents interferon (IFN)-beta-2a. This protein was used in the construction of a pharmaceutical composition which was used for treating inflammation, acute phase response, regulation of cell proliferation, inhibition of fibroblast proliferation and for prevention of sclerosis after infection. IFNs are important antiviral and antitumor proteins produced by the human body. The major species of IFN produced by human fibroblasts is IFN-beta-1. This is immunologically distinct from IFN-beta-2. Two genes have been found to encode IFN-beta-2, IFN-beta-2a and IFN-beta-2b.

CC encode IFN-beta-2, IFN-beta-2a and IFN-beta-2b.

CC Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;

Best Local Similarity 97.6%; Pred. No. 7.79e-111;

Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGDSKDVAAAPHRQPLTSERIDKQIRYI 60

QY 1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGDSKDVAAAPHRQPLTSERIDKQIRYI 60

Db 61 LDGISALRKETCNKSNMCSSKEALAEENLNLPKMAEKDGCFCFSGFNEETCLVKIITGLL 120

QY 61 LDGISALRKETCNKSNMCSSKEALAEENLNLPKMAEKDGCFCFSGFNEETCLVKIITGLL 120

Db 121 EFVYLEYLQNRFESEEQARAVOMSTKVLIQFLQKAKNLDATITPDPPTNASLTKLQ 180

QY 121 EFVYLEYLQNRFESEEQARAVOMSTKVLIQFLQKAKNLDATITPDPPTNASLTKLQ 180

Db 181 AQNWQDMTHLILRSFKFLOSLRALRQM 212

QY 181 AQNWQDMTHLILRSFKFLOSLRALRQM 212

RESULT 11

ID R05415 standard; protein; 212 AA.

AC R05415;

DT 27-JUL-1990 (first entry)

DE Human B-cell differentiation factor gene product.

KW BSF-2; dhfr; dihydrofolic acid reductase; differentiation.

OS Homo sapiens.

PN J02009388-A.

PD 12-JAN-1990.

PF 8-JUL-1988; 170142.

PR 9-MAR-1988; JP-055270.

PA (AJIN) Ajinomoto KK.

DR WPI: 90-055348/08.

DR N-PSDB: Q01763.

PT Physiologically active protein prepn. -

PT by transforming plasmid having gene coding physiologically active protein and gene of dihydrofolic acid reductase to hamster ovary etc.

PS Example 3; Fig 6; 12pp; Japanese.

CC Gene may be expressed by transforming a dhfr negative strain of CHO cells with an active BSF-2 gene and dhfr carrying vector. BSF-2 gene product is a B-cell differentiating factor.

CC is a B-cell differentiating factor.

CC Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;

Best Local Similarity 97.6%; Pred. No. 7.79e-111;

Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGDSKDVAAAPHRQPLTSERIDKQIRYI 60

QY 1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGDSKDVAAAPHRQPLTSERIDKQIRYI 60

Db 61 LDGISALRKETCNKSNMCSSKEALAEENLNLPKMAEKDGCFCFSGFNEETCLVKIITGLL 120

QY 61 LDGISALRKETCNKSNMCSSKEALAEENLNLPKMAEKDGCFCFSGFNEETCLVKIITGLL 120

Db 121 EFVYLEYLQNRFESEEQARAVOMSTKVLIQFLQKAKNLDATITPDPPTNASLTKLQ 180

QY 121 EFVYLEYLQNRFESEEQARAVOMSTKVLIQFLQKAKNLDATITPDPPTNASLTKLQ 180

Db 181 AQNWQDMTHLILRSFKFLOSLRALRQM 212

QY 181 AQNWQDMTHLILRSFKFLOSLRALRQM 212

RESULT 12

ID R49041 standard; protein; 212 AA.

AC R49041;

DT 06-SEP-1994 (first entry)

DE Human interleukin-6.

KW Interleukin 6; IL-6; thrombocytopoiesis; surgery; chemotherapy; radiation therapy; bone marrow transplantation; cancer therapy; neoplasia; anti-neoplastic activity.

KW neoplasia; anti-neoplastic activity.

OS Homo sapiens.

PN W09403492-A.

PD 17-FEB-1994.

PF 01-JUL-1993; A00324.

PR 06-AUG-1992; AU-003983.

PA (LUDW-) LUDWIG INST CANCER RES.

PA (UYME) UNIV MELBOURNE.

PI Simpson RJ Williams NT;

DR WPI: 94-065607/08.

DR N-PSDB: Q55973.

PT New interleukin-6 variants - capable of stimulating thrombocytopoiesis while exhibiting low hybridoma growth factor activity

PT activity

PS Disclosure; Page 33; 46pp; English.

CC This sequence is human interleukin-6 (IL-6). IL-6 variants in the form of non-full length molecules can stimulate, enhance or facilitate thrombocytopoiesis without the side effects of other IL-6 activities. The IL-6 variants are useful for inducing thrombocytopoiesis in thrombocytopenic patients following surgery. Chemotherapy, radiation therapy or bone marrow transplantation. The IL-6 variants may also be useful in cancer therapy where the fragments express anti-neoplastic activity.

CC IL-6 variants may also be useful in cancer therapy where the fragments express anti-neoplastic activity.

CC Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;
Best Local Similarity 97.6%; Pred. No. 7.79e-111;
Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
|||||
QY 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
|||||

Db 61 LDGIALRKETCNKNCMCSSKEALAEANNLNPMAEKDGCQFSGFNEETCLVKIITGLL 120
|||||
QY 61 LDGIALRKETCNKNCMCSSPEALAEANNLNPMAEKDGCQFSGFNEETCLVKIITGLL 120
|||||

Db 121 EFVYLEYLQNRFSSEEQARAVQSTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQ 180
|||||
QY 121 EFVYLEYLQNRFSSEEQARAVQSTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQ 180
|||||

Db 181 AQONWLODMTHLILRSKFQSSLRALROM 212
|||||
QY 181 AQONWLODMTHLILRSKFQSSLRALROM 212
|||||

RESULT 13
ID R34726 standard; protein; 212 AA.
AC R34726;
DE 24-AUG-1993 (first entry)
KW Human IL-6 (for modification).
OS Interleukin-6; stability; blood; cytokine; BSF-2.
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..29
FT protein /label= sig_pep
FT /label= mat_protein
PN J05086099-A.
PD 06-APR-1993.
PF 31-JUL-1991; 191475.
PR 31-JUL-1990; JP-204440.
PA (TORA) TORAY IND INC.
DR WPI; 93-149232/18.
PT Modified interleukin-6 derivs. - used to treat platelet-reducing conditions, thrombocytopenia
PS Claim 1; Page 2; 6pp; Japanese.
CC A modified interleukin-6 (IL-6) contg. at least 3 sequences of Asn-X-Thr or Asn-X-Ser, where X is an amino acid other than Pro, is claimed (no specific sequences, nor the sequence below are given in the specification 1).
CC The modified IL-6 can be expected to have higher stability in blood, higher medical effect and higher absorption in the objective organ.
CC Sequence 212 AA;
SQ

Query Match 97.4%; Score 1446; DB 1; Length 212;
Best Local Similarity 97.6%; Pred. No. 7.79e-111;
Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
|||||
QY 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
|||||

Db 61 LDGIALRKETCNKNCMCSSKEALAEANNLNPMAEKDGCQFSGFNEETCLVKIITGLL 120
|||||
QY 61 LDGIALRKETCNKNCMCSSPEALAEANNLNPMAEKDGCQFSGFNEETCLVKIITGLL 120
|||||

Db 121 EFVYLEYLQNRFSSEEQARAVQSTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQ 180
|||||
QY 121 EFVYLEYLQNRFSSEEQARAVQSTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQ 180
|||||

Db 181 AQONWLODMTHLILRSKFQSSLRALROM 212
|||||
QY 181 AQONWLODMTHLILRSKFQSSLRALROM 212
|||||

RESULT 14
ID P90371 standard; protein; 212 AA.
AC P90371;
DE 1-NOV-1989 (first entry)
DE PBSF2-L8
KW FC epsilon receptor; cloned gene; IgE; pBSF2-L8; allergy; asthma; BSF-2.
PN EP-321601-A.
PD 28-JUN-1989.
PF 22-DEC-1987; 119080.
PR 22-DEC-1987; EP-119080.
PA (OSAU) Osaka University.
PI Kishimoto T, Suemura M, Kikutani H, Barsumian E;
DR WPI; 89-186101/26.
DR N-PSDB; N90134, N90135, N90136.
FT Cloned genes coding for soluble IgE receptor - comprising modified coding sequence of Fc epsilon receptor gene.
PS Disclosure; fig 3; 19pp; English.
CC Peptide sequence of pBSF2-L8. See also N90134-6.
SQ Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;
Best Local Similarity 97.6%; Pred. No. 7.79e-111;
Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
|||||
QY 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
|||||

Db 61 LDGIALRKETCNKNCMCSSKEALAEANNLNPMAEKDGCQFSGFNEETCLVKIITGLL 120
|||||
QY 61 LDGIALRKETCNKNCMCSSPEALAEANNLNPMAEKDGCQFSGFNEETCLVKIITGLL 120
|||||

Db 121 EFVYLEYLQNRFSSEEQARAVQSTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQ 180
|||||
QY 121 EFVYLEYLQNRFSSEEQARAVQSTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQ 180
|||||

Db 181 AQONWLODMTHLILRSKFQSSLRALROM 212
|||||
QY 181 AQONWLODMTHLILRSKFQSSLRALROM 212
|||||

RESULT 15
ID P81156 standard; protein; 212 AA.
AC P81156;
DE 10-MAR-1993 (revised)
DE 15-OCT-1990 (first entry)
DE Human B-cell differentiation factor (BCDF).
KW B-cell differentiation factor; BCDF; cancer; autoimmune.
OS Homo sapiens.
PN EP-257406-A.
PD 2-MAR-1988.
PF 6-AUG-1988; 111409.
PR 06-AUG-1986; JP-184858.
PR 27-AUG-1986; JP-200433.
PR 18-DEC-1986; JP-302699.
PR 13-MAY-1987; JP-116332.
PA (AJIN) Ajinomoto KK.
PI Kishimoto TN, Hirano T, Matsui H, Takahara Y, Akiyama Y, Okano A;
DR WPI; 88-057698/09.
DR N-PSDB; N81460.
PT Purified polypeptide with B-cell differentiation factor activity - useful in prodn. of antibodies for diagnosis and therapy of cancers, infectious diseases etc.
PS Claim 24; Fig 5; 72pp; English.
CC BCDF may be used in the production and repair of B-cells, it is useful in treatment of autoimmune diseases, malignant tumors and may be used to influence B-cells to produce Abs in vitro.
CC Sequence 212 AA;
SQ

Query Match 97.2%; Score 1443; DB 1; Length 212;
Best Local Similarity 97.2%; Pred. No. 1.41e-110;
Matches 206; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Db 1 MNSFSTSAFGPYAFSLGLLVLPAAFPAPVPPGODSKDVAAPHROPLTSSERIDKOIRYI 60
    |||||||
Oy 1 MNSFSTSAFGPYAFSLGLLVLPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKOIRYI 60
    |||||||
Db 61 LDGIALRKRETCNKSNCESSEKALAEENNLPKMAEKDGCFOSGFNEETCLVKIITGIL 120
    |||||||
Oy 61 LDGIALRKRETCNKSNCESSEKALAEENNLPKMAEKDGCFOSGFNEETCLVKIITGIL 120
    |||||||
Db 121 EEEVYLEYLONRFESSESEQARA VOMSTKVLIOFLQKKAKNDAITTPPTNASLITKLQ 180
    |||||||
Oy 121 EEEVYLEYLONRFESSESEQARA VOMSTKVLIOFLQKKAKNDAITTPPTNASLITKLQ 180
    |||||||
Db 181 AONOWLODMTHLILRSFEKFILOSSLRALROM 212
    |||||||
Oy 181 AONOWLODMTHLILRSKEFLQSLRALROM 212
    |||||||
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